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RESULT 2
CS098022 38059 bp DNA linear PAT 03-JUN-2005
LOCUS Sequence 4 from Patent WO2000075279.
DEFINITION CS098022
ACCESSION CS098022.1 GI:66954267
VERSION
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Kurachi, K. and Kurachi, S.
TITLE Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL Patent: WO 2000075279-A 4 14-DEC-2000;
The Regents of the University of Michigan (US)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1703; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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LOCUS AR390767
DEFINITION Sequence 4 from patent US 6610906.
ACCESSION AR390767
VERSION AR390767.1 GI:40113109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38059)
AUTHORS Kuzachi, K. and Kuzachi, S.
TITLES Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL Patent: US 6610906-A 4 26-AUG-2003; Ann Arbor, MI
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Query Match 99.7%; Score 1701.8; DB 6; Length 38059;
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RESULT 4
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LOCUS AX409478
DEFINITION Sequence 2125 from Patent WO0229103.
ACCESSION AX409478
VERSION AX409478.1 GI:21442183
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Alvaraz, C., Horne, D., Perez-da-Silva, S. and Vockley, J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 2125 11-APR-2002;
JOURNAL GENE LOGIC INC (US)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1703; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATGAAGATGAGATTTTCCAGGTAATTCATGGAATTTGAATTAACAGGCGCTCTCAC 60
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RESULT 5
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LOCUS Human coagulation factor IX gene, complete cds.
DEFINITION K02402.1 GI:182612
ACCESSION K02402.1
VERSION 1
KEYWORDS Ali repeat; Christmas factor; KpnI repetitive sequence; antihemophilic factor B; factor IX; repeat region; sample repetitive sequence.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 38059)
Yoshitake, S., Schach, B. G., Foster, D. C., Davie, B. W. and Kurachi, K. Nucleotide sequence of the gene for human factor IX (antihemophilic factor B)
Biochemistry 24 (14), 3736-3750 (1985)
JOURNAL PUBMED 2994716
REFERENCE 2 (bases 23487 to 23556)
Rees, D. J., Rizza, C. R. and Brownlee, G. G. Hemophilia B caused by a point mutation in a donor splice junction of the human factor IX gene
Nature 316 (6029), 643-645 (1985)
JOURNAL PUBMED 4033760
REFERENCE 3 (bases 23378 to 23387)
Graham, J. B., Lubahn, D. B., Lord, S. T., Kirshtein, J., Nilsson, I. M., Wallmark, A., Ljung, R., Piazier, L. D., Ware, J. L., Lin, S. W., Stafford, D. W. and Boeco, J. The Malmo polymorphism of coagulation factor IX, an immunologic polymorphism due to dimorphism of residue 148 that is in linkage disequilibrium with two other F.IX polymorphisms
Am. J. Hum. Genet. 42 (4), 573-580 (1988)
JOURNAL PUBMED 2450455
REFERENCE 4 (bases)
Hirosewa, S., Fahner, J. B., Sailer, J. P., Wu, C. T., Lowyten, E. and Kurachi, K. Structural and functional basis of the developmental regulation of human factor IX gene: factor IX Leyden
Unpublished (1990)
JOURNAL COMMENT Original source text: Homo sapiens (clone: FIX-lambda-[6,36,53,61]) (Clisue library: T.Maniatis et al.) DNA; and Homo sapiens (clone: FIX-lambda-4243) DNA. Sequence for [1] kindly submitted on floppy by K. Kurachi, 05-AUG-1985.

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[1] notes a potential TATA box (2939-2942) and polyadenylation signal (35701-35706); and notes two start codons (downstream of the start codon annotated below) that may be alternative and/or preferred starts for the factor IX prepropeptide. Several tracts of simple repetitive sequence are present [1], including regions with the potential for hairpin and/or Z-DNA formation. [1] describes six long open reading frames in the intron and on the complementary strand.

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AUTHORS	Rieder,M.U., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A., Rajkumar,N.R., Toth,B.J., Yi,Q. and Nickerson,D.A.
TITLE	Direct Submission
JOURNAL	Submitted (07-AUG-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT	To cite this work please use: SeattleSNPs. NHLBI HL66682 Program for Genetic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).
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QY	1441	TGATGATGATGAGGACATACGACAAATATCATCTGACCCGTCGACAGCTGCTCCTTCC	1500
Db	34366	TGATGATGATGAGGACATACGACAAATATCATCTGACCCGTCGACAGCTGCTCCTTCC	34425

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OY      1501  TGCCCAACATCAACCCCAAGCAGCCCTCACTCTGGCTAGTTCCTTAGTCTTTTAGTC 1560
Db      34426  TGCCCAACATCAACCCCAAGCAGCCCTCACTCTGGCTAGTTCCTTAGTCTTTTAGTC 3448
OY      1561  AATATATATTTTGTCTTGGCATATAGTATTAATAAACAATATTTTAAATTTCTTGCGCTGG 1620
Db      34486  AATATATATTTTGTCTTGGCATATAGTATTAATAAACAATATTTTAAATTTCTTGCGCTGG 3454
OY      1621  GCCCAGTGGCTCAGCCCTTATATCCCACTCTTGGAGGCCAAGGTGGGATCACT 1680
Db      34546  GCCCAGTGGCTCAGCCCTTATATCCCACTCTTGGAGGCCAAGGTGGGATCACT 3460
OY      1681  GAGGTTAGAGTTTTCAGGCGAAGCT 1705
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RESULT 7
HS88D7
LOCUS      158557 bp      DNA      linear      PRI 18-MAY-2005
DEFINITION      Human DNA sequence from clone Rpe-88D7 on chromosome Xq25-26.3
Containing the P9 gene for P9: coagulation factor IX (plasma
thromboplastic component, Christmas disease, hemophilia B) (FIX,
PTC, HEMB) and the 3' end of the MCF2 gene for MCF.2 cell line
derived transforming sequence (DBL), complete sequence.
AL033403
AL033403.1 GI:3859054
HTG; DBL; P9; FIX; HEMB; MCF2; PTC.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eumetazoa; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 158557)
Bird,C.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: veg@sanger.ac.uk
Clone requests: clonerequests@sanger.ac.uk
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em; EMBL; Sw; SWISSPROT; Tr; TrEMBL; Wp; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
Rpe-88D7 is from the library RPe1-6 constructed by the group of
Pletier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pPAC4
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: veg@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
Location/Qualifiers
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Query Match	98.7%	Score 1684.6	DB 8	Length 158557					
Best Local Similarity	99.6%	Pred. No. 0							
Matches 1699	Conservative 0	Mismatches 4	Indels 2	Gaps 1					
OY	1	AAATGAAGATGAGATTTTCCAGCTTTAATTCATATGGAATTGAAATTAACAGGGCCCTCAC	60						
Db	35389	AAATGAAGATGAGATTTTCCAGCTTTAATTCATGGAATTGAAATTAACAGGGCCCTCAC	35444						
OY	61	TAACTAATCACTTCCCATCTTTTGTAGATTGAAATATATACATTCATGATCATTTGCT	120						
Db	35449	TAACTAATCACTTCCCATCTTTTGTAGATTGAAATATATACATTCATGATCATTTGCT	35550						
OY	121	TTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGACCAATTTGATGAAATGGA	180						
Db	35509	TTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGACCAATTTGATGAAATGGA	35566						
OY	181	CCACTAAGGAATATATATGTTAGAGAAATTAAGTACATTTCTAAGGGCCAGCCCTTGA	240						
Db	35569	CCACTAAGGAATATATATGTTAGAGAAATTAAGTACATTTCTAAGGGCCAGCCCTTGA	3562						
OY	241	CAAAATGTGAAGTTAATTTCTCCACTCTGTCCATCAGATACATATGSGTTCTCACTATNG	300						
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OY	301	CAACTAATCTCATATTTTCCCTCTTAGACAGATTCATCTTCCGATCTTCTTGCT	360						
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OY	361	TTCTCCAAACCAAAACATGAATGTTATATAGTTCTGTATACAGATCAGGATCTTGGTCTAC	420						
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OY	421	TCATACCAAGGCCAGTACACACTCATGGAAGAAAGAACAGAGATAGCTGAGAGGCTA	480						
Db	35809	TCATACCAAGGCCAGTACACACTCATGGAAGAAAGAACAGAGATAGCTGAGAGGCTA	3586						
OY	481	AAACTCATCAAAAACACTACTCCTTTTCTGTACCTTATCTCTAATCTTTTACTTTTC	540						
Db	35869	AAACTCATCAAAAACACTACTCCTTTTCTGTACCTTATCTCTAATCTTTTACTTTTC	3592						
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Db	35929	CAATCCCATTTCCCAATCAATGTTTTCTCTTTCTTACCTCCCTCTCCCTTTTAACTCTC	3598						
OY	601	CATGTCGTTTAAAGAGAGATGGGAGACATATTTCTGTATATCTTCTGTACACAGTTATA	660						
Db	35989	CATGTCGTTTAAAGAGAGATGGGAGACATATTTCTGTATATCTTCTGTACACAGTTATA	3604						
OY	661	CATGTCATCAAAACCCAGACTTGTCTTCATATGTGGAACCTTGCTTTCAAGAACATAAGGA	720						
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Db	36227	TATGCGTGCTGTGAGACACACGCGATACACATATATATGGAAGCAATAGCCATTTCTA	3628						
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Db	36287	AGACCTGTATATGTTATGAGAGGTGTGACTGTGGCATGATTTTCAAGAGGCAAGATTGGCAT	3634						
OY	961	ATCATTTGTAATCAAAAAGCTGACATTTGACCCGACATATTTGTACTCTTTCTAATAATAA	1020						
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RESULT 10
HUMCIX LOCUS 2775 bp mRNA linear PRI 01-NOV-1994
DEFINITION Human coagulation factor IX mRNA, complete cde.
ACCESSION M11309
VERSION M11309.1 GI:180552
KEYWORDS clotting factor; clotting factor IX; coagulation factor;
coagulation factor IX; factor IX.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominales; Homo.
REFERENCE 1 (bases 1 to 2775)
McGraw, R.A., Davis, L.M., Noyes, C.M., Lundblad, R.L., Roberts, H.R.,
Graham, J.B. and Stefford, D.W.
Evidence for a prevalent dimorphism in the activation peptide of
human coagulation factor IX
Proc. Natl. Acad. Sci. U.S.A. 82 (9), 2847-2851 (1985)
JOURNAL PUBMED 3857619
TITLE 2 (bases 214 to 222; 313 to 321; 877 to 885)
Chen, S.H., Thompson, A.R., Zhang, M. and Scott, C.R.
Three point mutations in the factor IX gene of five hemophilia B
patients: identification strategy using localization by altered
epitopes in their hemophilic proteins
J. Clin. Invest. 84 (1), 113-118 (1989)
JOURNAL PUBMED 2472424
TITLE Original
COMMENT source text: Human liver cDNA to mRNA.
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316
variation
variation

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variation      580
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ORIGIN      Chromosome Xq26.3-q27.2.

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Beet Local Similarity 100.0%; Pred. No. 2e-271;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 AATGAAGATGATGATTCAGAGTTAATTCATGGAATGAAATTAACAGGGCCCTCTAC 60
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Oy      61 TAACTAATCACTTCCATCTTTTGTAGATTGAAATTAATCAATTCATGATCTCT 120
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Oy      241 CAAATTTGGAAGTTAAATTTCTCACTCTGTCATCAATCAATGTTTCTCACTANG 300
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Oy      301 CAACTAATCTGCTGAATTTTCCCTCCTTAGAGAGATTCATCTTCCGATCTCTTGT 360
Db      1685 CAACTAATCTGCTGAATTTTCCCTCCTTAGAGAGATTCATCTTCCGATCTCTTGT 1744

Oy      361 TCTCCACCAAAACATCATGTTTATTAAGTTCTGTATACAGTACAGATCTTGTCTAC 420
Db      1745 TCTCCACCAAAACATCATGTTTATTAAGTTCTGTATACAGTACAGATCTTGTCTAC 1804

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Oy      481 AAACATCAAAAACATCACTCTTCTCTACCTTCTCAATCTCTTCTTACCTTTTC 540
Db      1865 AAACATCAAAAACATCACTCTTCTCTACCTTCTCAATCTCTTCTTACCTTTTC 1924

Oy      541 CAAATCCCAATCCCAAAATCAAGTTTCTCTTCTTACTCTCTCTCTCTCTTCTTAC 600
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Oy      601 CATGTCGTTAAAGAGATGAGAGATGAGATCTCTGTTATACCTTCTGTAACAGTTATA 660
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Oy      721 TGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTCTTTCAGAGATTAATATTT 780
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Oy      781 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 840
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RESULT 11

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G28615      2775 bp DNA linear STS 11-JUL-1996
LOCUS      human STS SHGC-35785, sequence tagged site.
DEFINITION      G28615
ACCESSION      G28615.1 GI:11408430
VERSION      STS; STS sequence; primer; sequence tagged site.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Hukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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      1 (bases 1 to 2775)
      Myers, R.M.
      Unpublished (1996)
REFERENCE      Contact: Richard M. Myers
      Stanford Human Genome Center (SHGC)
      Stanford University School of Medicine
      Department of Genetics, M-344, Stanford, CA 94305, USA
      Tel: 4157259687
      Fax: 4157259689
      Email: myers@shgc.stanford.edu
AUTHORS      JOURNAL
COMMENT

```

Primer A: GTAGGTGCTGAAAAGTTTGG
 Primer B: GTGAATCATGCTAGTCAGACC
 STS size: 219
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol: Template: 25 ng

Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer: MgCl₂: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M11309
-- Washington University/Merck EST sequence.

FEATURES

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ORIGIN

Query Match 81.5%; Score 1391; DB 10; Length 2775;

Best Local Similarity 100.0%; Pred. No. 2e-271;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAAAGATGATTCAGAGTTAATTCATTGAAATGAAATTAACAGGGCCCTCAC 60
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CO882048

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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Isogenis, Inc. (US)

Location/Qualifiers

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Q1.Y., Zhang X. and Konigsberg P.J.
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RESULT 13

AR452580

LOCUS

DERIVATION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

1 (bases 1 to 2804)
 Beignt, D.W., Craft, T.J., Francisovich, J.B., Goodson, T. Jr.,
 Hail, S.E., Hertton, D.K., Kinkowski, V.J., Masters, J.J., Mendel, D.,
 Milot, G., Sawyer, J.S., Shuman, R.T., Smith, G.F., Tebbe, A.L.,
 Timley, J.M., Weir, L.C., Wikel, J.H., Wiley, M.R. and Lee, T.K.
 Antithrombotic agents
 Patent: US 6677369-A 2 13-JAN-2004;
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13: geneseqn2010s:*
14: geneseqn2011s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	100.0	1707	6	AA171008 Human Fac
2	1701.8	99.7	38059	4	AAFS4018 Human fac
3	1701.8	99.7	38059	6	ABN95627 Gene #212
4	1701.8	99.7	38059	10	ADDP1098 Human coa
5	1391	81.5	2775	3	AAAS4034 Human fac
6	1391	81.5	2804	8	ABV77053 Nucleoid
7	1387.8	81.3	2792	2	AAK28626 Nucleoid
8	1385.6	81.2	2781	1	AAW40142 Part of t
9	1384.2	81.1	2802	2	AAAT02460 Human Fac
10	1379.2	80.8	2781	1	AAWA0177 Part of t
11	1376.6	80.6	2728	13	ADQ38340 Human SNP
12	1376.6	80.6	2771	13	ADQ38338 Human SNP
13	1376.6	80.6	2777	13	ADQ38339 Human SNP
14	1376.6	80.6	2831	13	ADQ38341 Human SNP
15	1373.4	80.5	2758	13	ACN43105 Human dia
16	1373.4	80.5	2766	13	ACN43104 Human dia
17	1292	75.7	2807	13	AAAN60543 Factor-IX
18	1292	75.7	2807	12	ADHA42198 Novel hum
19	1273	74.6	1273	4	AAFS4017 hFIX gene

20	1272	74.5	1272	4	AAFS4080	AAFS4080 hFIX gene
21	1271.4	74.5	1273	4	AAFS4074	AAFS4074 hFIX gene
22	1271.4	74.5	1273	4	AAFS4073	AAFS4073 hFIX gene
23	1269.8	74.4	1273	4	AAFS4075	AAFS4075 hFIX gene
24	1266.6	74.2	1273	4	AAFS4076	AAFS4076 hFIX gene
25	1261	73.9	1272	4	AAFS4079	AAFS4079 hFIX gene
26	1261	73.9	1275	4	AAFS4077	AAFS4077 hFIX gene
27	1260	73.8	1276	4	AAFS4078	AAFS4078 hFIX gene
28	933.4	54.7	1971	4	ABAS5251	ABAS5251 Human Itoe
29	933.4	54.7	1971	4	ABAS28575	ABAS28575 Human Itoe
30	236	13.8	1438	6	ABQ82328	ABQ82328 Human NOV
31	236	13.8	1438	12	ADH42196	ADH42196 Novel hum
32	236	13.8	1638	1	AAAS0351	AAAS0351 Sequence
33	236	13.8	1639	1	AAAS0049	AAAS0049 Sequence
34	236	13.8	1639	1	AAAS0362	AAAS0362 Sequence
35	203.8	11.9	1612	13	ADH42200	ADH42200 Novel hum
36	200.6	11.8	201	13	ADQ40547	ADQ40547 Myocardia
37	200.6	11.8	201	13	ADQ40266	ADQ40266 Myocardia
38	200.6	11.8	201	13	ADQ40829	ADQ40829 Myocardia
39	200.6	11.8	201	13	ADQ41116	ADQ41116 Myocardia
40	172.4	10.1	422	8	ABX47596	ABX47596 Bovine BS
41	160	9.4	1610	2	AAH88061	AAH88061 Human IGF
42	159	9.4	13928	4	AAH77500	AAH77500 Haemophil
43	159	9.3	1548	2	AAQ81549	AAQ81549 Factor-IX
44	159	9.3	1548	2	AAQ76017	AAQ76017 Human Fac
45	159	9.3	1548	2	AAH88292	AAH88292 Human Fac

ALIGNMENTS

RESULT 1
AA171008
ID AA171008 standard; DNA; 1707 BP.
XX
AC AA171008;
DT 18-MAR-2002 (first entry)
DE Human Factor IX gene 3' untranslated region.
XX
KW Factor IX, human; expression cassette; liver; blood clotting;
KW gene therapy; 3' untranslated region; 3' UTR; ds.
OS Homo sapiens.
XX
PM MO200198482-A2.
PD 27-DEC-2001.
XX
PF 19-JUN-2001; 2001WO-US019634.
XX
PR 20-JUN-2000; 2000US-0212902P.
XX
XX (STRD) UNIV IELAND STANFORD JUNIOR.
XX (UNIW) UNIV WASHINGTON.
XX
XX Miao CH, Kay MA;
XX WPI; 2002-114582/15.
XX
XX Nucleic acid construct for expressing nucleic acid molecules, proteins in
XX mammalian liver cells, has operably linked hepatic locus control element,
XX hepatic promoter, coding sequence, polyadenylation signal and intron.
XX
XX Example 1; Page 57-59; 64pp; English.
XX
XX The present sequence is that of the 3' untranslated region (3' UTR) of
XX the human Factor IX gene. The 3' UTR, which includes a polyadenylation
XX signal. It was incorporated into expression cassettes of the invention
XX that were designed for liver-specific expression of Factor IX. The
XX cassettes also include a hepatic locus control element, an hepatic
XX promoter located 3' to the hepatic locus control element, a Factor IX

CC coding sequence, and an intron (see A171003-16). Also provided are
 CC vectors that include an expression cassette of the invention. These may
 CC episomal or integrating vectors, including viral vectors, and are used in
 CC a claimed method of ameliorating disease. A therapeutic amount blood
 CC clotting factor IX is produced in mammalian liver cells for at least 100
 CC days, and preferably at least 500 days. In examples of the invention,
 CC human factor IX was expressed in mouse liver cells following infection of
 CC retrovirus-based plasmids that carried the expression cassettes into the
 CC tail vein or portal vein, and by direct injection of plasmid DNA into the
 CC liver

XX Sequence 1707 BP; 500 A; 362 C; 305 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1707; DB 6; Length 1707;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAAAGATGATTTCCAGGTTAATTCATGGAATGGAATTAAGAGGCTTCAC 60
 DB 1 AATGAAAGATGATTTCCAGGTTAATTCATGGAATGGAATTAAGAGGCTTCAC 60
 QY 61 TAACTAATCACTTCCCATCTTGTGTAGATTGAAATATATACATTCATGATGCT 120
 DB 61 TAACTAATCACTTCCCATCTTGTGTAGATTGAAATATATACATTCATGATGCT 120
 QY 121 TTTTCTCTTAAAGGGGAAATTTTCATATTTTACCTGAGCAATGATTGAAATGGA 180
 DB 121 TTTTCTCTTAAAGGGGAAATTTTCATATTTTACCTGAGCAATGATTGAAATGGA 180
 QY 181 CCACTAGAGAAATTAATGTTGAGAAATACAGTCAATTCATGAGGCGCCGCTTGA 240
 DB 181 CCACTAGAGAAATTAATGTTGAGAAATACAGTCAATTCATGAGGCGCCGCTTGA 240
 QY 241 CAATATGTAAGTAAATTCCTCACTCTGTCATGATGATGATGCTTCCACTAGG 300
 DB 241 CAATATGTAAGTAAATTCCTCACTCTGTCATGATGATGATGCTTCCACTAGG 300
 QY 301 CAATTAATCACTGATTTTCCCTCTGAGAGATTCATCTTCCGATCTTCTTGGCT 360
 DB 301 CAATTAATCACTGATTTTCCCTCTGAGAGATTCATCTTCCGATCTTCTTGGCT 360
 QY 361 TCTTCAACCAAAACATCAATGTTTATAGTCTGTATACAGTACAGGATCTTGGTAC 420
 DB 361 TCTTCAACCAAAACATCAATGTTTATAGTCTGTATACAGTACAGGATCTTGGTAC 420
 QY 421 TCTATCAAGAGGCGAGTACCACTCACTAGAGAAAGAACAGAGTACGTAGAGCTA 480
 DB 421 TCTATCAAGAGGCGAGTACCACTCACTAGAGAAAGAACAGAGTACGTAGAGCTA 480
 QY 481 AATCTCATCAAAACACTATCTCTTCTCTGTAACCTTATCTGAAATCTTTTACCTTTC 540
 DB 481 AATCTCATCAAAACACTATCTCTTCTCTGTAACCTTATCTGAAATCTTTTACCTTTC 540
 QY 541 CAATATCCCAATCCCAATCAATGTTTCTCTTCTTACCTCTCCCTCTTTTACCTTC 600
 DB 541 CAATATCCCAATCCCAATCAATGTTTCTCTTCTTACCTCTCCCTCTTTTACCTTC 600
 QY 601 CATGTCGTTAAAGAGAGATGAGGAGCATCTTCTGTATACCTTCTGTAACAAGTATA 660
 DB 601 CATGTCGTTAAAGAGAGATGAGGAGCATCTTCTGTATACCTTCTGTAACAAGTATA 660
 QY 661 CATGTCATCAAAACCAAGACTTGTCTTCATAGTGAAGACTTGTCTTTCAGAACTAGGA 720
 DB 661 CATGTCATCAAAACCAAGACTTGTCTTCATAGTGAAGACTTGTCTTTCAGAACTAGGA 720
 QY 721 TGAAGTAAAGTGCCTGAAAAGTTGGGGAAAAGTTCTTTCAGAGAGTTAAGTTATTT 780
 DB 721 TGAAGTAAAGTGCCTGAAAAGTTGGGGAAAAGTTCTTTCAGAGAGTTAAGTTATTT 780
 QY 781 AT 840
 DB 781 AT 840

QY 841 TATGCTGTGTGTAGACACACACGCAATACATATATATATATATATATATATATATAT 900
 DB 841 TATGCTGTGTGTAGACACACACGCAATACATATATATATATATATATATATATATAT 900
 QY 901 AGAGCTGTATGTATATAGAGTGTGACTAGGATGATTTTCAGAGGCAAGATTGGCAT 960
 DB 901 AGAGCTGTATGTATATAGAGTGTGACTAGGATGATTTTCAGAGGCAAGATTGGCAT 960
 QY 961 ATCATTTGTAT 1020
 DB 961 ATCATTTGTAT 1020
 QY 1021 TAAATATATATCTTACAGAAAGAAAGAACACCTGTTGCTTATCTACAGTATAGAGA 1080
 DB 1021 TAAATATATATCTTACAGAAAGAAAGAACACCTGTTGCTTATCTACAGTATAGAGA 1080
 QY 1081 CTTTGAAGAGAAATTCACAGTGTGTCTTACAGAGTGTGAGGCAAGAAAGTTGA 1140
 DB 1081 CTTTGAAGAGAAATTCACAGTGTGTCTTACAGAGTGTGAGGCAAGAAAGTTGA 1140
 QY 1141 AGTTCCTTACAGAGAGACATATATATATATATATATATATATATATATATATATAT 1200
 DB 1141 AGTTCCTTACAGAGAGACATATATATATATATATATATATATATATATATATATAT 1200
 QY 1201 GAGAGGCTGACAGAGCTCAAGAGCATATAGTATTCATTCAGCCCACTAAGTGTCT 1260
 DB 1201 GAGAGGCTGACAGAGCTCAAGAGCATATAGTATTCATTCAGCCCACTAAGTGTCT 1260
 QY 1261 TTTCTGTTTGTGTGTACCAAGGAAATTTTATATATATATATATATATATATATATAT 1320
 DB 1261 TTTCTGTTTGTGTGTACCAAGGAAATTTTATATATATATATATATATATATATATAT 1320
 QY 1321 CTTCTAGAGAGTGTCTGACCAATGATGATTTTCCCTTGTGAAATTAATTAATCTGGTG 1380
 DB 1321 CTTCTAGAGAGTGTCTGACCAATGATGATTTTCCCTTGTGAAATTAATTAATCTGGTG 1380
 QY 1381 TTTCTGTTTGT 1440
 DB 1381 TTTCTGTTTGT 1440
 QY 1441 TGAATGATGATGAGGAGCTACTGCAAAATCACTGACCCCTGCAAGCTGTGCTTCTCC 1500
 DB 1441 TGAATGATGATGAGGAGCTACTGCAAAATCACTGACCCCTGCAAGCTGTGCTTCTCC 1500
 QY 1501 TGCCCCAATCTCAACCCCAAGGAGGCTCACTCTGTAGTCTTGTAGTCTTGTAGTCT 1560
 DB 1501 TGCCCCAATCTCAACCCCAAGGAGGCTCACTCTGTAGTCTTGTAGTCTTGTAGTCT 1560
 QY 1561 AATATATATTTTGTCTGTGCAATATATATATATATATATATATATATATATATATAT 1620
 DB 1561 AATATATATTTTGTCTGTGCAATATATATATATATATATATATATATATATATATAT 1620
 QY 1621 GCCCAGTGTGCTCAGGCTATATATCCAGCACTTCTGAGGCAAGGTCGAGTACCT 1680
 DB 1621 GCCCAGTGTGCTCAGGCTATATATCCAGCACTTCTGAGGCAAGGTCGAGTACCT 1680
 QY 1681 GAGGTTAGAGTTTCAAGGCCAAGCTTA 1707
 DB 1681 GAGGTTAGAGTTTCAAGGCCAAGCTTA 1707

RESULT 2

AAF54018 standard; DNA; 38059 BP.

AAF54018;

30-MAR-2001 (first entry)

Human factor IX (hFIX) gene, SEQ ID NO:4.

Age-related gene regulation; liver-specific; gene expression;
 human factor IX; hFIX; AB5'; AB3'; age-regulatable expression construct;

KM antisense therapy; gene therapy; thrombosis; cardiovascular disease;
 KW diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
 XX osteoarthritis; dementia; ds.
 OS Homo sapiens.
 PN WO200075279-A2.
 PD 14-DEC-2000.
 PF 06-JUN-2000; 2000WO-US015728.
 XX
 XX
 PR 09-JUN-1999; 99US-00328925.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PI Kurachi K, Kurachi S;
 DR WPI; 2001-061708/07.
 XX P-PSDS; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60286,
 DR AAB60287, AAB60288, AAB60289.
 XX
 PT New regulatory elements that control age-related gene expression, useful
 PT in gene therapy and for reducing Factor IX expression.
 PS
 PS Disclosure; Fig 9A-B; 225pp; English.
 CC The invention relates to nucleic acid sequences which regulate gene
 CC expression in an age-related manner and/or in a liver-specific manner.
 CC The invention identifies regions of the human factor IX (hFIX) gene, and
 CC a region of the human protein C (hPC) gene, which are age-related
 CC regulatory sequences. The hFIX age-related regulatory sequences are
 CC designated AB5' (AAFs44016) and AB3' (AAFs44017), and are found in the 5'
 CC UTR (at position 2164-2165 of AAFs44018) and 3' UTR (at position 34383-
 CC 35655 of AAFs44018) respectively. These elements act synergistically to
 CC increase hFIX levels over the lifespan of an individual; however, they
 CC can independently exert effects on hFIX mRNA in an age-related manner,
 CC with AB5' acting to stabilise hFIX mRNA, and AB3' acting to increase hFIX
 CC mRNA levels, over time. AB5' also directs liver-specific expression. The
 CC hPC gene age-related regulatory sequence is found in the 5' UTR
 CC 5'-GAGGAAA-3' and contains two PBA-3 (polyoma virus activator 3) elements
 CC 5'-GAGGAAA-3' and 5'-CAGCAGAG-3'. The age-related regulatory sequences of
 CC the invention, along with their homologues, variants and fragments, may
 CC be used in the construction of recombinant expression vectors for the
 CC expression of a desired sequence in an age-related fashion in a host
 CC cell. Preferred target genes for expression in such age-regulatable
 CC expression vectors include those encoding proteins involved in blood
 CC coagulation (e.g., the pro-coagulant factor IX and factor VIII, and the
 CC anti-coagulant protein C and antithrombin III), human alpha-1-
 CC antitrypsin, PBA-3 protein and reporter proteins such as luciferase.
 CC Preferred promoters for use in such age-regulatable expression vectors
 CC include the human factor IX promoter, the T7 promoter, the T3 promoter
 CC and the S6 promoter. The expression vectors of the invention may be used
 CC in gene therapy to provide age- related and/or liver-specific expression
 CC of target genes. Age-regulatable constructs may be used in the treatment
 CC of such age-related conditions such as thrombosis, cardiovascular
 CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
 CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
 CC to express factor IX antisense mRNA in the treatment of thrombotic
 CC conditions associated with the natural age-related rise in factor IX
 CC expression. Transgenic cells or animals that contain vectors of the
 CC invention are useful as models of these diseases, in screening for
 CC potential therapeutic agents and for studying normal processes such as
 CC ageing and gene expression. Fragments and homologues of age-related
 CC regulatory sequences, are useful as probes to detect, isolate or identify
 CC other such sequences in samples. The present sequence represents the hFIX
 CC gene
 SQ Sequence 38059 BP; 12326 A; 7397 G; 7441 G; 10895 T; 0 U; 0 Other;

[illegible]

QY	1081	CTTTGAGGAAATTTCAAAGTGTGTTTCAAGCAGTGTTCAGAGCCAAAGAAATTGA	1140
Db	35413	CTTTGAGGAAATTTCAAAGTGTGTTTCAAGCAGTGTTCAGAGCCAAAGAAATTGA	35472
QY	1141	AGTTCCTTAGACCAAGAGCATTAAGTATGTCCTCTTAACTAGCATACCCGAAGTG	1200
Db	35473	AGTTCCTTAGACCAAGAGCATTAAGTATGTCCTCTTAACTAGCATACCCGAAGTG	35522
QY	1201	GAGAAAGGTGACAGAGCTCAAAGGCGATTAGTCAATTCAGCCAACTAAGTGTCT	1260
Db	35533	GAGAAAGGTGACAGAGCTCAAAGGCGATTAGTCAATTCAGCCAACTAAGTGTCT	35592
QY	1261	TTTCTGTTTCGTGTTTCACCAATGAGCAATTTGATTAATAGTTATCCTTATCTTGAA	1320
Db	35593	TTTCTGTTTCGTGTTTCACCAATGAGCAATTTGATTAATAGTTATCCTTATCTTGAA	35652
QY	1321	CTTCTTAAGAGTGTCTGACCACTGAGGTATGTTCCCTTGTGAAATTAATAACCTGTG	1380
Db	35653	CTTCTTAAGAGTGTCTGACCACTGAGGTATGTTCCCTTGTGAAATTAATAACCTGTG	35712
QY	1381	TTCTGTTCATATACCTTGAGCTTTTGTGAGATTCAATGATGATGATCAACCTGTAT	1440
Db	35713	TTCTGTTCATATACCTTGAGCTTTTGTGAGATTCAATGATGATGATCAACCTGTAT	35772
QY	1441	TGATGATGCAATGAGACTAGTCAAAATCACTGACCTTGCAAGCTGTGCTTCTCC	1500
Db	35773	TGATGATGCAATGAGACTAGTCAAAATCACTGACCTTGCAAGCTGTGCTTCTCC	35832
QY	1501	TGCCCCAAGCTCAACCCCGACGAGGCTCATCTGTGCTAGTTCCTTATGCTTTAAGTC	1560
Db	35833	TGCCCCAAGCTCAACCCCGACGAGGCTCATCTGTGCTAGTTCCTTATGCTTTAAGTC	35892
QY	1561	AATATATTTTGTCTTCGCATATTAAGTATTAATAATATTTTAAATTTCTTGCTGG	1620
Db	35893	AATATATTTTGTCTTCGCATATTAAGTATTAATAATATTTTAAATTTCTTGCTGG	35952
QY	1621	GCCCAAGTGTCTACGCTTATTAATCCAGCACTTCTGGAAGCCAAAGTGGGCGATCACT	1680
Db	35953	GCCCAAGTGTCTACGCTTATTAATCCAGCACTTCTGGAAGCCAAAGTGGGCGATCACT	36012
QY	1681	GAGGTTAGAGTTTCAGGCGCAAGCT	1705
Db	36013	GAGGTTAGAGTTTCAGGCGCAAGCT	36037
RESULT 3			
ABN95627			
ID	ABN95627	standard; DNA; 38059 BP.	
AC	ABN95627;		
XX			
DT	13-AUG-2002	(first entry)	
XX			
Db	Gene #2125 used to diagnose liver cancer.		
XX			
KV	Gene; liver cancer; dr; hepatocellular carcinoma; hepatotropic;		
KW	metastatic liver tumour; cytostatic; expression profile; disease state;		
XX	disease progression; drug toxicity; drug efficacy; drug metabolism.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200229103-A2.		
PD	11-APR-2002.		
XX			
PP	02-OCT-2001; 2001WO-US030589.		
XX			
PR	02-OCT-2000; 2000US-0237054P.		
XX			
PA	(GENE-) GENE LOGIC INC.		
XX			
PI	Horne D, Alvares C, Peres-Da-Silva S, Vockley JG,		
XX			

DR	MPI; 2002-426119/45.
XX	
PT	Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
PT	
XX	
PS	Claim 1; SEQ ID NO 2125; 298pp; English.
CC	
XX	
CC	The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytoskeletal activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
CC	
CC	
CC	
CC	
CC	
SQ	Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;
Query Match	99.7%; Score 1701.8; DB 6; Length 38059;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1703; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1 AATGAAAGATGATTTTCGAAGTAAATCTATTGGAAATGAAAATTAACAGGGCCTCAC 60
DB	AATGAAAGATGATTTTCGAAGTAAATCTATTGGAAATGAAAATTAACAGGGCCTCAC 34393
OY	61 TAACTATCACTTCCCATCTTTGTGTAGATTGAATATATACATTCATGATCGCT 120
DB	TAACTATCACTTCCCATCTTTGTGTAGATTGAATATATACATTCATGATCGCT 34393
OY	121 TTTTCTCTTTACAGGGGAAATTCATATTTCCTGAGCAATGATTGAAAAATGAA 180
DB	TTTTCTCTTTACAGGGGAAATTCATATTTCCTGAGCAATGATTGAAAAATGAA 34512
OY	34453 TTTTCTCTTTACAGGGGAAATTCATATTTCCTGAGCAATGATTGAAAAATGAA 34512
OY	181 CCAGTAGAGAATAATATGTTAGAGAAATTAAGTCATTTCTAAGGGCCAGCCCTTGA 240
DB	CCAGTAGAGAATAATATGTTAGAGAAATTAAGTCATTTCTAAGGGCCAGCCCTTGA 34513
OY	241 CAAAATTTGTAAGTAAATCTCCACTCTGTGCATGAGTACTAGTGTTCTCCACTAG 300
DB	CAAAATTTGTAAGTAAATCTCCACTCTGTGCATGAGTACTAGTGTTCTCCACTAG 34573
OY	301 CAACTAATCACTCACTATTTTCCCTCCTTAGACAGCATTCATCTTCCGATCTTTGGCT 360
DB	CAACTAATCACTCACTATTTTCCCTCCTTAGACAGCATTCATCTTCCGATCTTTGGCT 34633
OY	361 TTCACAACCAAACATCAATGTTATTAGTTCGTATACAGTACAGAGATCTTTGGCTAC 420
DB	TTCACAACCAAACATCAATGTTATTAGTTCGTATACAGTACAGAGATCTTTGGCTAC 34693
OY	421 TCTATCAACAAGGCCAGTACCACACTCATGAAGAAACAACAGAGTACTGAGAGCTTA 480
DB	TCTATCAACAAGGCCAGTACCACACTCATGAAGAAACAACAGAGTACTGAGAGCTTA 34753
OY	481 AAATCATCAAAAACACTACTCTTTTCCCTTACAGCTATTTCCCATCTTTTACCTTTTC 540
DB	AAATCATCAAAAACACTACTCTTTTCCCTTACAGCTATTTCCCATCTTTTACCTTTTC 34813
OY	541 CAATCCCAATCCCAGAAATCAGTTTTCCTTTCTTACTCCCTCTCCCTTTAACCTTC 600
DB	CAATCCCAATCCCAGAAATCAGTTTTCCTTTCTTACTCCCTCTCCCTTTAACCTTC 34873
OY	601 CATGTCGCTTAAAGAGAGATGGGGAGCATCATTCGTATATCTCTGACACAGTTATA 660
DB	CATGTCGCTTAAAGAGAGATGGGGAGCATCATTCGTATATCTCTGACACAGTTATA 34933

[illegible]

RESULT 4
ADD71098 ID ADD71098 standard; DNA; 38059 BP.
XX AC
XX ADD71098;
XX 15-JAN-2004 (first entry)
XX Human coagulation factor IX gene SEQ ID NO:102.
XX liver cancer; chronic hepatitis; cirrhosis; liver disease; hepatotropic;
XX cytosolic; gene therapy; human; gene; de.
XX Homo sapiens.
XX MO2003061564-A2.
XX 31-JUL-2003.
XX 20-DEC-2002; 2002MO-US040718.
XX 21-DEC-2001; 2001US-0341815P.
XX 31-DEC-2001; 2001US-0343185P.
XX (GENE-) GENE LOGIC INC.
XX (LGBI-) LG BIOMEDICAL INST.
XX Koh SS, Liu Q, Chung H, Zeng W, Lee B, Yeremilli S, Song SY;
XX MPI; 2003-663343/62.
XX
XX Diagnosing liver cancer cells, useful for treating liver cancer
XX associated with chronic hepatitis or cirrhosis comprises detecting the
XX level of expression in a tissue sample of one or more genes associated
XX with cancerous liver tissues.
XX
XX Claim 1; SEQ ID NO 102; 176pp; English.
XX
XX The present invention describes a method for diagnosing liver cancer
XX cells comprising detecting the level of expression in a tissue sample of
XX one or more genes given in the specification (see ADD70997 to ADD71105),
XX where differential expression of the genes is indicative of liver cancer.
XX Also described: (1) detecting the progression of liver cancer in a
XX patient; (2) monitoring the treatment of a patient with liver cancer; (3)
XX treating a patient with liver cancer; (4) typing a liver disease in a
XX patient; (5) detecting the presence or progression of liver cancer in a
XX patient with chronic hepatitis or cirrhosis; (6) differentiating liver
XX cancer related to chronic hepatitis from liver cancer related to
XX cirrhosis; (7) screening for an agent capable of modulating the onset or
XX progression of liver cancer; (8) a composition comprising at least two
XX oligonucleotides comprising a sequence that specifically hybridizes to
XX any of the genes; (9) a solid support comprising the at least two
XX oligonucleotides; (10) a computer system comprising a database containing
XX information identifying the level in liver tissue of a set of genes; (11)
XX a method for using the computer system to present information identifying
XX the expression level in tissue or cell of any of the genes; and (12) a
XX therapeutic agent for slowing or halting the progression of liver cancer.
XX The methods are useful for treating liver cancer associated with chronic
XX hepatitis or cirrhosis. The present sequence represents a specifically
XX claimed human gene sequence which is used in the exemplification of the
XX present invention.
XX
XX Seq 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;
XX
XX Query Match 99.7%; Score 1701.8; DB 10; Length 38059;
XX Best Local Similarity 99.9%; Pct. No. 0;
XX Matches 1703; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AATGAAAGATGATTTTCAAGGTTAATTCATTGGAAATTAACAGGGCCCTCAAC 60
XX 34333 AATGAAAGATGATTTTCAAGGTTAATTCATTGGAAATTAACAGGGCCCTCAAC 34332

QY 61 TAACTAATCACTTTCCATCTTTGTAGATTGAAATATATACATTTATGATCTTCT 120
 Db 34393 TAACTAATCACTTTCCATCTTTGTAGATTGAAATATATACATTTATGATCTTCT 34452
 QY 121 TTTTCTCTTTACAGGGAGAAATTTCAATTTTACCTGAGCAATGATTAGAAATGGA 180
 Db 34453 TTTTCTCTTTACAGGGAGAAATTTCAATTTTACCTGAGCAATGATTAGAAATGGA 34512
 QY 181 CCACATGAGAAATATATATGTTAGAAATTAACATCTATTTCTAGGGCCAGCCCTTGA 240
 Db 34513 CCACATGAGAAATATATGTTAGAAATTAACATCTATTTCTAGGGCCAGCCCTTGA 34572
 QY 241 CAAATTTGTGAAGTAAATTTCTCACTCTCTCCATCAATATATATATGTTCTCAATAG 300
 Db 34573 CAAATTTGTGAAGTAAATTTCTCACTCTCTCCATCAATATATATATGTTCTCAATAG 34632
 QY 301 CAACATCACTCACTCAATTTTCCCTCTTACAGCAATCTCTCCCATCTTCTTGTCT 360
 Db 34633 CAACATCACTCACTCAATTTTCCCTCTTACAGCAATCTCTCCCATCTTCTTGTCT 34692
 QY 361 TCTCCAAACCAAAACATCAATGTTTATATGTTCTGTATACATGATCAAGATCTTGTCTAC 420
 Db 34693 TCTCCAAACCAAAACATCAATGTTTATATGTTCTGTATACATGATCAAGATCTTGTCTAC 34752
 QY 421 TCTATCAAGGCGAGTACCACTCACTGAGAAAGAAACACAGAGATAGCTGAGAGCTA 480
 Db 34753 TCTATCAAGGCGAGTACCACTCACTGAGAAAGAAACACAGAGATAGCTGAGAGCTA 34812
 QY 481 AAATCTATCAAAACACATCTCTCTTCTCTACCTTATCTCAATCTTTTACCTTTC 540
 Db 34813 AAATCTATCAAAACACATCTCTCTTCTCTACCTTATCTCAATCTTTTACCTTTC 34872
 QY 541 CAAATCCCAATCCCAATCAATGTTTCTCTTCTTCTCTCTCTCTCTCTCTTTCACCTTC 600
 Db 34873 CAAATCCCAATCCCAATCAATGTTTCTCTTCTTCTCTCTCTCTCTCTCTTTCACCTTC 34932
 QY 601 CATGCTGTAAAGAGAGATGAGGAGATCATCTGTATATCTTCTGTACACAGTATA 660
 Db 34933 CATGCTGTAAAGAGAGATGAGGAGATCATCTGTATATCTTCTGTACACAGTATA 34992
 QY 661 CATGCTATCAAAACCAAGACTTGTCTCATATGAGAGACTTGTCTTACAGAACATAGGA 720
 Db 34993 CATGCTATCAAAACCAAGACTTGTCTCATATGAGAGACTTGTCTTACAGAACATAGGA 35052
 QY 721 TGAAGTAAAGGCTCTGAAAAGTTTGGGGGAAAAGTTTCTTACAGAGATTATTTT 780
 Db 35053 TGAAGTAAAGGCTCTGAAAAGTTTGGGGGAAAAGTTTCTTACAGAGATTATTTT 35112
 QY 781 AT 840
 Db 35113 AT 35172
 QY 841 TATGCTGTGTGTAGACACACAGCATACACATATATATGAAAGCAATAGCATTTCTA 900
 Db 35173 TATGCTGTGTGTAGACACACAGCATACACATATATATGAAAGCAATAGCATTTCTA 35232
 QY 901 AGAGCTGTATGTTATGAGAGGTCTGACTAGGCAATTTTCAAGAGGCAAGATTGGCAT 960
 Db 35233 AGAGCTGTATGTTATGAGAGGTCTGACTAGGCAATTTTCAAGAGGCAAGATTGGCAT 35292
 QY 961 ATCATTTGTAATTAAGGCTGACATTTGACCCAGACATTTGTAATTTCTTCTTAAATTA 1020
 Db 35293 ATCATTTGTAATTAAGGCTGACATTTGACCCAGACATTTGTAATTTCTTCTTAAATTA 35352
 QY 1021 TAAATATATATGTTTAAAGAAAGAGAACGTTTCTTCAATCTTACAGCTAGTAGAGA 1080
 Db 35353 TAAATATATATGTTTAAAGAAAGAGAACGTTTCTTCAATCTTACAGCTAGTAGAGA 35412
 QY 1081 CTTTGAAGAAAGATTCAACAGTGTCTTCAAGAGTCTTCAAGCCCAAGCAAGATTGA 1140
 Db 35413 CTTTGAAGAAAGATTCAACAGTGTCTTCAAGAGTCTTCAAGCCCAAGCAAGATTGA 35472
 QY 1141 AGTTGCTAGACGAGAGCATATAGTATCTCTTTAACTAGATATCCCGAAGTG 1200

Db 35473 AGTTGCTAGACGAGAGCATATAGTATCTCTTTAACTAGATATCCCGAAGTG 35532
 QY 1201 GAGAGGGGTGACAGAGCTCAAGAGCAATAGTCAATTCACCACTCAAGTTGTCT 1260
 Db 35533 GAGAGGGGTGACAGAGCTCAAGAGCAATAGTCAATTCACCACTCAAGTTGTCT 35592
 QY 1261 TTTCTGTTTGTGTTCACATGAGAACATTTGATATATATATATATATATATATATATAT 1320
 Db 35593 TTTCTGTTTGTGTTCACATGAGAACATTTGATATATATATATATATATATATATATAT 35652
 QY 1321 CTTCTAGAGGTTGCTGACCAATGAGATGTTTCCCTTGTGAAATTAATTAACGTG 1380
 Db 35653 CTTCTAGAGGTTGCTGACCAATGAGATGTTTCCCTTGTGAAATTAATTAACGTG 35712
 QY 1381 TTTCTGTTTACCTTGTGCTTTTGTGATTCATATGATGATCACTCACTTAT 1440
 Db 35713 TTTCTGTTTACCTTGTGCTTTTGTGATTCATATGATGATCACTCACTTAT 35772
 QY 1441 TGATGATGATGAGATCTGACAAATCACTGACCTTGCACAGCTGCTTCTCC 1500
 Db 35773 TGATGATGATGAGATCTGACAAATCACTGACCTTGCACAGCTGCTTCTCC 35832
 QY 1501 TGCCCAACCTCAACCCCAAGGCTCACTCTGCTAGTCTTCTTATGTC 1560
 Db 35833 TGCCCAACCTCAACCCCAAGGCTCACTCTGCTAGTCTTCTTATGTC 35892
 QY 1561 AATATATTTTGTCTTGTGAT 1620
 Db 35893 AATATATTTTGTCTTGTGAT 35952
 QY 1621 GCCCAGTGTCTACAGCTTATATATCCAGCACTTCTGAGGCAAGGTGGCGGATCACT 1680
 Db 35953 GCCCAGTGTCTACAGCTTATATATCCAGCACTTCTGAGGCAAGGTGGCGGATCACT 36012
 QY 1681 GAGGTAGAGTTTCAAGGCCAGCT 1705
 Db 36013 GAGGTAGAGTTTCAAGGCCAGCT 36037

RESULT 5
 ID AAA54034 standard; DNA; 2775 BP.
 AC AAA54034;
 XX 08-FEB-2001 (first entry)
 DT XX
 DE Human factor IX coding sequence.
 XX
 XX Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein;
 KW fusion protein; coagulation factor; Factor X; Factor VII; Protein S;
 KW Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human;
 KM de.
 XX
 OS Homo sapiens.
 XX
 PN MO200054787-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 16-MAR-2000; 2000MO-US006934.
 XX
 PR 16-MAR-1999; 99US-0124609P.
 XX
 PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
 XX (UNNC-) UNIV NORTH CAROLINA.
 XX
 PI High KA, Camire RM, Larson PJ, Stafford DW;
 XX
 DR WPI; 2000-638152/61.
 XX
 PT Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent

protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the protein.

Disclousure; Fig 6D-11; 60pp; English.

Efficient processing and release of mature two-chain factor X into the circulation requires: removal of the signal sequence; formation of disulfide bonds; modification of amino terminal glutamic acid residues, to gamma-carboxyglutamic acid; modification of one aspartic acid in the first epidermal growth factor (EGF) domain to beta-hydroxyaspartic acid; addition of N- and O-linked oligosaccharides to the activation peptide; removal of an internal tripeptide to yield two-chain factor X and removal of the propeptide just prior to secretion. While some of these modifications do not appear essential for factor X function the removal of the signal sequence, propeptide, internal tripeptide and full gamma-carboxylation are all steps which are important requisites for the production of biologically active factor X/FXa. Isolated chimeric polynucleotides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin K-dependent protein (VDP). The fusion proteins encoded are vitamin K-dependent protein gamma-carboxylation enhancers and are useful for optimizing the gamma-carboxylation of a VKDP to produce a fully gamma-carboxylated VKDP. The fusion proteins and recombinant cells expressing them are useful for alleviating a VKDP associated disease. The fusion constructs result in the production of fully gamma-carboxylated mature VKDPs, which are biologically active. The invention encompasses all combinations of propeptide sequences (modified or not) and VKDP's. This sequence encodes the signal, propeptide and mature protein sequence of human Factor IX

Sequence 2775 BP; 859 A; 528 C; 564 G; 824 T; 0 U; 0 Other;

Query Match 81.5%; Score 1391; DB 3; Length 2775;

Best Local Similarity 100.0%; Pred. No. 2.6e-282;

Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AATGAAGATGATTTCCAGGTTAATTCATTTGAATGAATTAACAGGCGCTCTCAC 60
 1385 AATGAAGATGATTTCCAGGTTAATTCATTTGAATGAATTAACAGGCGCTCTCAC 1444
 61 TAACTAATCACTTTCCATCTTTTGTATGATTTGAATTAATTAATCAATCTTGTCT 120
 1445 TAACTAATCACTTTCCATCTTTTGTATGATTTGAATTAATTAATCAATCTTGTCT 1504
 121 TTTTCTCTTTCAGGGGGAATTCATATTTTAACTGAGCAATGATTAGAAATGGA 180
 1505 TTTTCTCTTTCAGGGGGAATTCATATTTTAACTGAGCAATGATTAGAAATGGA 1564
 181 CCACTAGAGAAATATATGTGTAGAAATTAAGTCAATTTCTAAGGGCCAGCCCTTGA 240
 1565 CCACTAGAGAAATATATGTGTAGAAATTAAGTCAATTTCTAAGGGCCAGCCCTTGA 1624
 241 CAAAATGTGAATTAATTTCTCACTGTGTCATCAATCAATCAATCAATCAATCAAT 300
 1625 CAAAATGTGAATTAATTTCTCACTGTGTCATCAATCAATCAATCAATCAATCAAT 1684
 301 CAACTAATCACTCAATTTTCCCTTACAGAGATTCATCCGATCTCTTGTCT 360
 1685 CAACTAATCACTCAATTTTCCCTTACAGAGATTCATCCGATCTCTTGTCT 1744
 361 TCTCCACCAAAATCATCAATGTTTATAGTCTGTATACAGTACAGATCTTTGTCTAC 420
 1745 TCTCCACCAAAATCATCAATGTTTATAGTCTGTATACAGTACAGATCTTTGTCTAC 1804
 421 TCTATCAAGGCGCGTACACATCACTAGAGAAAGAACACAGAGTGTAGAGGCTA 480
 1805 TCTATCAAGGCGCGTACACATCACTAGAGAAAGAACACAGAGTGTAGAGGCTA 1864
 481 AACTCATCAAAATCACTACTCTTTCTCTACCTATCTCTCAATCTTTTACCTTTTC 540
 1865 AACTCATCAAAATCACTACTCTTTCTCTACCTATCTCTCAATCTTTTACCTTTTC 1924
 541 CAATCCCAATCCCAATCAATGTTTCTCTTTTACTCTCTCTCTCTTTTACCTTC 600

1925 CAAATCCCAATCCCAATCAATGTTTCTCTTTTACTCTCTCTCTCTTTTACCTTC 1984
 601 CATGCTGTAAAGAGATGGAGACATCTCTGTATATCTCTGTACACAGTTATA 660
 1985 CATGCTGTAAAGAGATGGAGACATCTCTGTATATCTCTGTACACAGTTATA 2044
 661 CATGCTGTAAAGAGATGGAGACATCTCTGTATATCTCTGTACACAGTTATA 720
 2045 CATGCTGTAAAGAGATGGAGACATCTCTGTATATCTCTGTACACAGTTATA 2104
 721 TGAAGTAAAGTGTCTGAAAGATTTGGGGGAAAGTTCTTCAAGAGTTAATTTT 780
 2105 TGAAGTAAAGTGTCTGAAAGATTTGGGGGAAAGTTCTTCAAGAGTTAATTTT 2164
 781 AT 840
 2165 AT 2224
 841 TATGCTGTGTAGACACACACCATACACATATATATATATATATATATATATATAT 900
 2225 TATGCTGTGTGTAGACACACACCATACACATATATATATATATATATATATATAT 2284
 901 AGAGCTGTATGTAT 960
 2285 AGAGCTGTATGTAT 2344
 961 ATCATGTGTAT 1020
 2345 ATCATGTGTAT 2404
 1021 TAT 1080
 2405 TAT 2464
 1081 CTTTGAAGAAATTTCAACAGTGTCTTCAAGAGTTTCAAGAGTTTCAAGAGTTTCAAG 1140
 2465 CTTTGAAGAAATTTCAACAGTGTCTTCAAGAGTTTCAAGAGTTTCAAGAGTTTCAAG 2524
 1141 AGTTCCTAGACACAGAGACATTAAGTATCATGTCTCTTTTAACTAGCATACCCGAA 1200
 2525 AGTTCCTAGACACAGAGACATTAAGTATCATGTCTCTTTTAACTAGCATACCCGAA 2584
 1201 GAGAAAGGTGACAGAGCTCAAGAGCATTAAGTATCATTAATCAATCAATCAATCAAT 1260
 2585 GAGAAAGGTGACAGAGCTCAAGAGCATTAAGTATCATTAATCAATCAATCAATCAAT 2644
 1261 TTTTGT 1320
 2645 TTTTGT 2704
 1321 CTTTGAAGAGTTGTGACCAATGACATGATGTTTCCCTTGTGTAATTAATTAATTAAT 1380
 2705 CTTTGAAGAGTTGTGACCAATGACATGATGTTTCCCTTGTGTAATTAATTAATTAAT 2764
 1381 TTTGT 1440
 2765 TTTGT 1504

RESULT 6

ABV77053 standard; DNA; 2804 BP.

ABV77053;

03-MAR-2003 (first entry)

Nucleotide sequence of human Factor IX.

Factor VIII; non-viral vesicle vector; vesicular membrane; hepatitis B; envelope protein; Factor IX; liver cell; gene therapy; haemophilia; gene; 88.

	Homo sapiens.	Location/Qualifiers
OS		
XX		
PH	Key	30..1415
PT	CDS	/tag=a
FT		/product= "Factor IX"
XX		
PN	MO200286091-A2.	
XX		
PD	31-OCT-2002.	
XX		
PE	25-APR-2002; 2002WO-US03164.	
XX		
PR	25-APR-2001; 2001US-0286314P.	
XX		
PA	(RBGC) UNIV CALIFORNIA.	
XX		
P1	Chien KR, Hoshijima M;	
XX		
MP1	WPI; 2003-093125/08.	
DR	P-FSDB; ABB9529.	
XX		
PT	New non-viral vesicle vector comprises vesicular membrane with hepatitis B envelope protein and nucleic acid expression construct comprising complete factor VIII or IX coding sequence, useful for treating hemophilia.	
PT		
XX		
PS	Disclosure; Page 19-21; 34pp; English.	
XX		
CC	The present sequence encodes a human Factor IX. Factor IX polynucleotides are used to construct non-viral vesicle vectors. These vectors comprise a vesicular membrane with hepatitis B envelope protein exposed on the vesicle surface, and a nucleic acid expression construct comprising a complete factor VIII or factor IX coding sequence and a promoter sequence functional in liver cells. The non-viral vesicle vector is useful in gene therapy protocols for treating haemophilia	
CC		
CC		
CC		
CC		
CC		
CC		
CC		
SO	Sequence 2804 BP, 868 A; 536 C; 568 G; 832 T; 0 U; 0 Other;	
Query Match	81.5%; Score 1391; DB 8; Length 2804;	
Best Local Similarity	100.0%; Pred. No. 2,6e-282;	
Matches 1391; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 AATGAAGAGTGGATTTCGAAAGTTTAATCATTTGAATTAACAGAGGCCCTTGAC 60	
Db	1414 AATGAAGAGTGGATTTCGAAAGTTTAATCATTTGAATTAACAGAGGCCCTTGAC 1473	
OY	61 TAACATACTCATTCCCATCTTTGTGTAGATTGAAATATATACATTCATATGATCAATGCT 120	
Db	1474 TAACATACTCATTCCCATCTTTGTGTAGATTGAAATATATACATTCATATGATCAATGCT 1533	
OY	121 TTTTCTCTTTAAGGGGGAATTCATATTTTACTGAGCAATGATTAGAATAATGGAA 180	
Db	1534 TTTTCTCTTTAAGGGGGAATTCATATTTTACTGAGCAATGATTAGAATAATGGAA 1593	
OY	181 CCACTAGAGGAATTAATGTGTGGGAATTAACAGTCACTTTCTAAGGGCCGAGCCCTTGA 240	
Db	1594 CCACTAGAGGAATTAATGTGTGGGAATTAACAGTCACTTTCTAAGGGCCGAGCCCTTGA 1653	
OY	241 CAATAATGTGAAGTTAAATTTCCACTGTGTCATCAGATATATATGTTCTCCAATATG 300	
Db	1654 CAATAATGTGAAGTTAAATTTCCACTGTGTCATCAGATATATATGTTCTCCAATATG 1713	
OY	301 CAACATACTCACTCAATTTTCCCTCCCTAGAGCAATTCACATTCGCCGATCTTCTTGCT 360	
Db	1714 CAACATACTCACTCAATTTTCCCTCCCTAGAGCAATTCACATTCGCCGATCTTCTTGCT 1773	
OY	361 TTCTCAAACAATAATCATATGTTTATAGTCTGTATATACAGTACAGATCTTTGGTCTAC 420	
Db	1774 TTCTCAAACAATAATCATATGTTTATAGTCTGTATATACAGTACAGATCTTTGGTCTAC 1833	
OY	421 TCATATCACAGGCCAGTACCACACTCATGAAGAAAAGAACAGAGATGACTGAAGGCTTA 480	

[illegible]

[illegible]

QY	301	CACTAACTCACTCAATTTTCCCTCTTAGACGACATTCGACATCCCGACATCTCTTGGT	360
Db	1702	CAACTAACTCACTCAATTTTCCCTCTTAGACGACATTCGACATCCCGACATCTCTTGGT	1765
QY	361	TTCTCAACCAAAACATCAATGTTATTAGTCTGTATACAGTACAGATCTTTGGTCTAC	420
Db	1762	TTCTTAACCAAAACATCAATGTTATTAGTCTGTATACAGTACAGATCTTTGGTCTAC	1822
QY	421	TCATACAGAGCCAGTACCACTCATGAGAAAGAAACAAGAGTAGCTGAGAGCTTA	480
Db	1822	TCATACAGAGCCAGTACCACTCATGAGAAAGAAACAAGAGTAGCTGAGAGCTTA	1883
QY	481	AAACTCATCAAAAACATCACTCTCTTCTCTTACCTTACTCAATCTTTTACCTTTTC	540
Db	1882	AAACTCATCAAAAACATCACTCTCTTCTCTTACCTTACTCAATCTTTTACCTTTTC	1941
QY	541	CAAAATCCCAATCCCAATTCAGTTTCTCTTCTTCACTCCCTCTCCCTTATACCTTC	600
Db	1942	CAAAATCCCAATCCCAATTCAGTTTCTCTTCTTCACTCCCTCTCCCTTATACCTTC	2000
QY	601	CATGGTCGTTAAAGAGAGATGGGAGACATCTCTGTATATCTCTGTACAGATTATA	660
Db	2002	CATGGTCGTTAAAGAGAGATGGGAGACATCTCTGTATATCTCTGTACAGATTATA	2066
QY	661	CATGCTATCAAAACCCAGACTTCTCTCATAGTGGACATCTTCTTCAAGACATAGGGA	720
Db	2062	CATGCTATCAAAACCCAGACTTCTCTCATAGTGGACATCTTCTTCAAGACATAGGGA	2122
QY	721	TGAAGTAAAGTGGCCGAAAGATTGGGGGAAAAGTTCTTTCAGAGAGTTAAGTATTT	780
Db	2122	TGAAGTAAAGTGGCCGAAAGATTGGGGGAAAAGTTCTTTCAGAGAGTTAAGTATTT	2188
QY	781	ATAATATATATATATATATAAATAATATATATATATATATATATATATATATATAT	840
Db	2182	ATAATATATATATATATATAAATAATATATATATATATATATATATATATATATAT	2244
QY	841	TATGCGTGTGTATGACACACACCGATACACATATATATGAGACATTAAGCATTTCTA	900
Db	2242	TATGCGTGTGTATGACACACACCGATACACATATATATGAGACATTAAGCATTTCTA	2303
QY	901	AGAGCTTGTATATGTTATGAGAGTCTGATAGGACATTTTCAAGAGGCAAGATTGGCAT	960
Db	2302	AGAGCTTGTATATGTTATGAGAGTCTGATAGGACATTTTCAAGAGGCAAGATTGGCAT	2366
QY	961	ATCATTTGTACTTAAAAAAGCTGACATTTGACATTTGATCTCTTCTTAAATAATA	1020
Db	2362	ATCATTTGTACTTAAAAAAGCTGACATTTGACATTTGATCTCTTCTTAAATAATA	2422
QY	1021	TATATATATATGCTAACAGAAAGAAAGAGACCGTTCGTTTGCATTTACAGCTATAGAG	1080
Db	2422	TATATATATATGCTAACAGAAAGAAAGAGACCGTTCGTTTGCATTTACAGCTATAGAG	2488
QY	1081	CTTTGAGAGAAATTTCAACATGTGTCTTTCAGCAGTGTTCAGGCAAGCAAGATTGGA	1144
Db	2482	CTTTGAGAGAAATTTCAACATGTGTCTTTCAGCAGTGTGTTCAGGCAAGCAAGATTGGA	2544
QY	1141	AGTTCCTTAGACAGAGACATTAAGTATCATGTCTCTTTAACTAGCATACCCCGAAGTG	1200
Db	2542	AGTTCCTTAGACAGAGACATTAAGTATCATGTCTCTTTAACTAGCATACCCCGAAGTG	2600
QY	1201	GAGAAAGGTCGACGAGGCTCAAAAGGCATTAAGTCATTCGATCAGCCATTAAGTTGTCT	1260
Db	2602	GAGAAAGGTCGACGAGGCTCAAAAGGCATTAAGTCATTCGATCAGCCATTAAGTTGTCT	2666
QY	1261	TTTTCGTGTTTGTGTTCACATAGAAACATTTGATTAAGTTAAATCCCTCATCTTGAAT	1320
Db	2662	TTTTCGTGTTTGTGTTCACATAGAAACATTTGATTAAGTTAAATCCCTCATCTTGAAT	2722
QY	1321	CTTCTAGAGAGTGTCTGACCAACTGACGTATGTTTCCCTTGTGTGAATTAATAACCTG	1380
Db	2722	CTTCTAGAGAGTGTCTGACCAACTGACGTATGTTTCCCTTGTGTGAATTAATAACCTG	2788
QY	1381	TTCTGTGTTTCAT	1391

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Db      2782 TTTCTGTTTCAT 2792
|||||
RESULT 8
AA040142
ID      AA040142 standard; cDNA; 2781 BP.
XX
XX      AA040142;
AC
XX      25-MAR-2003 (revised)
DT      11-FEB-1992 (first entry)
XX
XX      Part of the sequence of human factor IX cDNA.
DB
XX      Christmas disease; therapy; haemophilia; factor IX; blood clotting;
KV      diagnosis; ss.
XX
XX      Homo sapiens.
OS
XX      Key
FH      sig_peptide      Location/Qualifiers
FT      21..143
FT      /*tag= a
FT      mat_peptide      144..1391
FT      /*tag= b
XX
XX      M08400560-A.
XX
XX      16-FEB-1984.
XX
XX      03-AUG-1983; 83MO-GB000191.
XX
XX      04-AUG-1982; 82GB-00022485.
XX      06-MAY-1983; 83GB-00012491.
XX
XX      (NATR ) NAT RES DEV CORP.
PA      (BROW/) BROWLER G G.
XX
XX      Brownlee G, Choo KH;
XX
XX      WPI; 1984-049331/08.
XX      P-PSDB; AAP40178.
XX
XX      Recombinant DNA cloning vehicles - useful in prodn. of factor IX
PT      polypeptide and of diagnostic probes for Christmas disease.
XX
XX      Example; Fig 9; 71pp; English.
XX
XX      The inventors claim DNA molecules comprising part or all of the human
CC      factor IX DNA. The invention also includes cDNA derived from human factor
CC      IX RNA. Specifically claimed are: recombinant DNA (the phage present in
CC      clone lambda Hix-1) deposited as NCIB No. 11749; Recombinant DNA in which
CC      the cloning vehicle is the modified PAR 153 plasmid present in E.coli
CC      NCIB No. 11747; Recombinant DNA in which the bovine factor IX cDNA
CC      sequence is contained in the recombinant DNA transformed into E.coli to
CC      form a clone deposited as NCIB No. 11748. (Updated on 25-MAR-2003 to
CC      correct PA field.)
XX
XX      Sequence 2781 BP; 859 A; 526 C; 567 G; 829 T; 0 U; 0 Other;
SQ
Query Match      81.2%; Score 1385.6; DB 1; Length 2781;
Best Local Similarity 99.7%; Pred. No. 3.6e-281;
Matches 1388; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      1 AATGAAGATGATGATTCGAAGTTAATTCATTCGATTCGAAATTAACAGGCTCTCAC 60
DB      1390 AATGAAGATGATTCGAAGTTAATTCATTCGATTCGAAATTAACAGGCTCTCAC 1449
QY      61 TAACTATATCACTTTCCATCTTTTGTAGATTGAATATATATACCTTATGATCATTTGCT 120
DB      1450 TAACTATATCACTTTCCATCTTTTGTAGATTGAATATATATACCTTATGATCATTTGCT 1509
QY      121 TTTTCTTTTACAGGGAGATTCATATTTTACCTGAGCAATGTGATGAAAATGGA 180

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DB      1510 TTTTCTTTTACAGGGAGATTCATATTTTACCTGAGCAATGTGATGAAAATGGA 1569
QY      181 CCACTAGAGAAATATATATGTTAGAAATTAACATCTATTTTAAGGCCGCCGCTTGA 240
DB      1570 CCACTAGAGAAATATATATGTTAGAAATTAACATCTATTTTAAGGCCGCCGCTTGA 1629
QY      241 CAAAATGTGAAAGTTAAATTCCTCACTCTGTCATGACATATCTATGTTTCCATATAG 300
DB      1630 CAAAATGTGAAAGTTAAATTCCTCACTCTGTCATGACATATCTATGTTTCCATATAG 1689
QY      301 CAATCACTCACTCAATTTTCCCTCTAGAGAAATTCATCTTCCGATCTTTGCT 360
DB      1690 CAATCACTCACTCAATTTTCCCTCTAGAGAAATTCATCTTCCGATCTTTGCT 1749
QY      361 TCTCCAAACCAAAATCAATATTTTATTTAGTTCTGTATACATGATGATCTTTGCTTAC 420
DB      1750 TCTCCAAACCAAAATCAATATTTTATTTAGTTCTGTATACATGATGATCTTTGCTTAC 1809
QY      421 TCTATCAAGAGCCAGTACCACTCATGAAAGAAACACAGAGTACGTAGAGCTTA 480
DB      1810 TCTATCAAGAGCCAGTACCACTCATGAAAGAAACACAGAGTACGTAGAGCTTA 1869
QY      481 AAATCTATCAAAACACTACTCTTTCTCTACCTTATCTCAATCTTTTACCTTTC 540
DB      1870 AAATCTATCAAAACACTACTCTTTCTCTACCTTATCTCAATCTTTTACCTTTC 1929
QY      541 CAATCCCAATCCCAATCATGTTTCTCTTCTTACCTCTCTCCCTTTTACCTTC 600
DB      1930 CAATCCCAATCCCAATCATGTTTCTCTTCTTACCTCTCTCCCTTTTACCTTC 1989
QY      601 CATGTCGTTAAGAGAGATGAGAGCATATCTGTATATCTTGTATACAGATTATA 660
DB      1990 CATGTCGTTAAGAGAGATGAGAGCATATCTGTATATCTTGTATACAGATTATA 2049
QY      661 CATGTCATCAAAACCACTACTCTTCTCATAGTGAAGACTTCTTCAAGAGATTATTT 780
DB      2050 CATGTCATCAAAACCACTACTCTTCTCATAGTGAAGACTTCTTCAAGAGATTATTT 2109
QY      721 TGAAGTAAAGTGTCTGAAAGATTTGGGGGAAAGTTCTTCAAGAGATTATTT 780
DB      2110 TGAAGTAAAGTGTCTGAAAGATTTGGGGGAAAGTTCTTCAAGAGATTATTT 2169
QY      781 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 840
DB      2170 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2229
QY      841 TATGCGTGTGTAGACACACAGCATATACATATATATATATATATATATATATATATAT 900
DB      2230 TATGCGTGTGTAGACACACAGCATATACATATATATATATATATATATATATATATAT 2289
QY      901 AGAGCTGTATGTTATGAGGTCTGACTAGCATGATTTCAAGAAAGCAAGATTGCGAT 960
DB      2290 AGAGCTGTATGTTATGAGGTCTGACTAGCATGATTTCAAGAAAGCAAGATTGCGAT 2349
QY      961 ATCATTTGATCTAAAGAGTGAACATTGACCCGACATATTTGATCTTTTAAAAATA 1020
DB      2350 ATCATTTGATCTAAAGAGTGAACATTGACCCGACATATTTGATCTTTTAAAAATA 2409
QY      1021 TAATATATATGCTACAGAAAGAAAGAACCGTTGCTTGCATCTACAGCTAGTAGAGA 1080
DB      2410 TAATATATATGCTACAGAAAGAAAGAACCGTTGCTTGCATCTACAGCTAGTAGAGA 2469
QY      1081 CTTTGAAGAAAGATTCAACAGTGTCTTTCAGAGTGTTCAGAGCCAGCAAGAGTTGA 1140
DB      2470 CTTTGAAGAAAGATTCAACAGTGTCTTTCAGAGTGTTCAGAGCCAGCAAGAGTTGA 2529
QY      1141 AGTTGCTTACAGAGAGCATATGATATATCTCTCTTAACTATACATATACCCGAGAG 1200
DB      2530 AGTTGCTTACAGAGAGCATATGATATATCTCTCTTAACTATACATATACCCGAGAG 2589
QY      1201 GAGAAGGATGACAGAGCTCAAGGATATAGTATTCATACAGCACTAAGATTGCTCT 1260

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Db 2590 GAGAGGGGTGACGAGCGCTCAAGGATTAAGTCAATTCACCACTTAGTTGCTT 2649
Qy 1261 TTCTGGTTGGTTCACGATGGAACATTTGATTAATGCTTATCTGAT 1320
Db 2650 TTCTGGTTGGTTCACGATGGAACATTTGATTAATGCTTATCTGAT 2709
Qy 1321 CTTCAGAGAGTTCCTGACCACTGACGTATGTTCCCTTGTGATTAATTAACGTG 1380
Db 2710 CTTCAGAGAGTTCCTGACCACTGACGTATGTTCCCTTGTGATTAATTAACGTG 2769
Qy 1381 TTCTGGTTGATA 1392
Db 2770 TTCTGGTTGATA 2781

RESULT 9
AAT02460 standard; mRNA, 2802 BP.
AAT02460;
AA02460;
15-APR-1996 (first entry)
Human Factor-IX mRNA.
Factor-IX; haemophilia; gene therapy; transgenic animal;
transgenic mouse; milk; cryptic splice site; PCR; primer;
polymerase chain reaction; ss.
Homo sapiens.
Key Location/Qualifiers
sfg_peptide 1..167
CDs 30..1415
mat_peptide 168..1412
misc_feature 1085
/note= "base 1085 is the cryptic donor site"
/tag= d
misc_feature 1547
/tag= e
/note= "base 1547 is the cryptic acceptor site"
W09530000-A1.
09-NOV-1995.
02-MAY-1995; 95MO-GB000996.
03-MAY-1994; 94GB-00008717.
(BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.
Clark AJ;
WPI; 1995-393074/50.
DNA expressing human factor IX having altered cryptic splice site - to
ensure high level expression of protein in transgenic hosts, esp. in
mammary glands, and for gene therapy of haemophilia.
Disclosure; Fig 21-21i; 28pp; English.
Human Factor-IX (FIX) mRNA (AAT02460) includes cryptic donor and acceptor
sites that cause a deletion of 462 nucleotides from FIX constructs
expressed in transgenic animals. Improved FIX sequences have at least 1
of these sites removed, so as to reduce or prevent the effects of
aberrant splicing and to increase FIX yields e.g. in milk. The improved
sequences may also be used in gene therapy

Query Match 81.1%; Score 1384.2; DB 2; Length 2802;
Best Local Similarity 68.1%; Pred. No. 7e-281;
Matches 946; Conservative 440; Mismatches 3; Indels 0; Gaps 0;
1 AATGAAAGATGATGATTTCCAGGTTAATTCATGGAATTTGAATTAACAGGCGCTCTAC 60
Db 1414 AATGAAAGATGATGATTTCCAGGTTAATTCATGGAATTTGAATTAACAGGCGCTCTAC 1473
Qy 61 TAACTAATCACTTCCCATCTTTTGTGATGATTTGAATTAATTAATTAATTAATTAAT 120
Db 1474 TAACTAATCACTTCCCATCTTTTGTGATGATTTGAATTAATTAATTAATTAATTAAT 1533
Qy 121 TTTCTCTTACAGGGGAGATTTCAATTTTACCTGACCAATTTGATTAATTAATTAAT 180
Db 1534 TTTCTCTTACAGGGGAGATTTCAATTTTACCTGACCAATTTGATTAATTAATTAATTAAT 1593
Qy 181 CCACTAGAGAAATTAATGATTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 1594 CCACTAGAGAAATTAATGATTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 1653
Qy 241 CAAATTTGAGAAATTAATTTCTCACTCTGTCATGATTAATTAATTAATTAATTAAT 300
Db 1654 CAAATTTGAGAAATTAATTTCTCACTCTGTCATGATTAATTAATTAATTAATTAATTAAT 1713
Qy 301 CAACTAATCACTCAATTTTCTCTTACGATTAATTAATTAATTAATTAATTAATTAAT 360
Db 1714 CAACTAATCACTCAATTTTCTCTTACGATTAATTAATTAATTAATTAATTAATTAATTAAT 1773
Qy 361 TCTGCAACCAAAATCAATGATTTTATGATTTCTGATTAATTAATTAATTAATTAATTAAT 420
Db 1774 TCTGCAACCAAAATCAATGATTTTATGATTTCTGATTAATTAATTAATTAATTAATTAAT 1833
Qy 421 TCTATCAAGAGCCAGTACCACTCACTGATTAATTAATTAATTAATTAATTAATTAAT 480
Db 1834 TCTATCAAGAGCCAGTACCACTCACTGATTAATTAATTAATTAATTAATTAATTAATTAAT 1893
Qy 481 AAATCTAATCAAAATCACTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCT 540
Db 1894 AAATCTAATCAAAATCACTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCT 1953
Qy 541 CAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 600
Db 1954 CAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 2013
Qy 601 CATGTCGTTAAAGAGATGAGGAGATCAATCTGATTAATTAATTAATTAATTAATTAAT 660
Db 2014 CATGTCGTTAAAGAGATGAGGAGATCAATCTGATTAATTAATTAATTAATTAATTAAT 2073
Qy 661 CATGTCATCAAAACCGAGCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCT 720
Db 2074 CATGTCATCAAAACCGAGCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCT 2133
Qy 721 TGAAGTAGAGTCTGAAAGATTTGGGGGAAAGTTCTTCTCTCAAGAGTTAATTAATTT 780
Db 2134 TGAAGTAGAGTCTGAAAGATTTGGGGGAAAGTTCTTCTCTCAAGAGTTAATTAATTT 2193
Qy 781 ATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
Db 2194 ATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2253
Qy 841 TATGCTGTGTGTGACACACGACATACACATTAATTAATTAATTAATTAATTAATTAAT 900
Db 2254 TATGCTGTGTGTGACACACGACATACACATTAATTAATTAATTAATTAATTAATTAAT 2313
Qy 901 AGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 2314 AGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2373
Qy 961 ATCAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Db 2374 ATCAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2433

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QY 1021 TAATATATATCTTAAACAGAAAGAGAAACCGTTCGTTGCAATCTACAGCTAGTAGAGA 1080
DB 2434 UAAUAAUUAUUGCUAACAGAAAGAGAAACCGUUGUUGCAUUCACAGCUAGUAGAGA 2493
QY 1081 CTTTGAAGAGAAATTCACAGTGTCTCTTCAGAGCTGTTTCAGAGCAAGAGAAAGTTGA 1140
DB 2494 CUUUGAGAGAAAUUCAAAGUGUGUCUUCAGAGUGUUCAGAGCAAGAGAAAGUUGA 2553
QY 1141 AGTTCCCTGACAGAGAGCAATTAAGTATCATGTCTCTTTAACTAGCATACCCGAAAGTG 1200
DB 2554 AGUCCCGAAGACAGAGAGCAUAAAGUACAUUGUCCUUAACUAGCAUACCCGAAAGUG 2613
QY 1201 GAGAAAGGTGACAGAGCTCAAGAGCATTAAGTCATTCATCAAGCAATTAAGTTCTCT 1260
DB 2614 GAGAAAGGTGACAGAGCTCAAGAGCATTAAGTCATTCATCAAGCAATTAAGTTCTCT 2673
QY 1261 TTTCTGTTTGTCTGTTTCCATGGAACATTTTGAATTAAGTAACTCTTCTTCTTGAAT 1320
DB 2674 UUUUCUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGU 2733
QY 1321 CTTCTAGAGAGTTCGTCGCAACTGACGTATGTTTCCCTTTGTAATTAATTAAGTGTG 1380
DB 2734 CUUUGAGAGAGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGU 2793
QY 1381 TTTCTGTTTCT 1389
DB 2794 UUCUGUGUUC 2802

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RESULT 10

AA0177
ID AA0177 standard; cDNA; 2781 BP.

AC AA0177;

DT 25-MAR-2003 (revised)
DT 13-FEB-1992 (first entry)

DX Part of the sequence of human factor IX cDNA.

XX Hemophilia; Christmas disease; diagnosis; treatment; ss.

OS Homo sapiens.

XX Key sig_peptide location/Qualifiers

FT 21.143

FT 94.257

FT 144.1391

FT 258.292

FT 397.525

FT 293.396

FT 144.1391

FT 258.292

FT 397.525

FT 293.396

FT 144.1391

FT 258.292

FT 397.525

FT 293.396

FT 144.1391

FT 258.292

FT 397.525

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PD 07-MAR-1984.
XX 03-AUG-1983; 83GB-00020975.
XX 04-AUG-1982; 82GB-00022486.
PR 16-MAY-1983; 83GB-00012490.
XX (NATR) NAT RES DEV CORP.
XX Brownlee GG, Choo KH;
XX WPI; 1984-057898/10.
DR P-PSDB; AAP40222.
PT Prodn. of artificial human factor IX - by use of recombinant DNA
PS sequences for host transformation and cultivation.
XX Example; Fig 9; 49pp; English.
XX The inventors claim a recombinant DNA having a human factor IX sequence
CC pref. at least 50 nucleotides long, esp. 75-2700 nucleotides. A cloning
CC vector contg. foreign DNA is also claimed. The foreign sequence pref.
CC includes the whole of an exon sequence of the human factor IX genome. The
CC cloning vehicle may be a modified pMT 153 plasmid. Also claimed is a
CC labeled diagnostic probe comprising a DNA molecule having a single- or
CC double-stranded probe sequence of 15 to 1000 nucleotides long factor IX
CC DNA sequence. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 2781 BP; 861 A; 531 C; 563 G; 826 T; 0 U; 0 Other;

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Query Match 80.8%; Score 1379.2; DB 1; Length 2781;
Best Local Similarity 99.4%; Pred. No. 7.9e-280;
Matches 1384; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1 AATGAAGATGATTTTCAAGGTTAATTCATGGAATTAAGAAATTAACAGGGCTCTAC 60
DB 1390 AATGAAGATGATTTTCAAGGTTAATTCATGGAATTAAGAAATTAACAGGGCTCTAC 1449
QY 61 TAACTATACCTTCCATCTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 1450 TAACTATACCTTCCATCTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1509
QY 121 TTTTCTTTTACAGGGAGAAATTTCAATTTTACCTGAGCAATTAATTAATTAATTAATTAAT 180
DB 1510 TTTTCTTTTACAGGGAGAAATTTCAATTTTACCTGAGCAATTAATTAATTAATTAATTAAT 1569
QY 181 CCACTAGAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 1570 CCACTAGAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1629
QY 241 CAAATTTGTAAGTTAATTTCTCACTCTGTCATGATTAATTAATTAATTAATTAATTAATTA 300
DB 1630 CAAATTTGTAAGTTAATTTCTCACTCTGTCATGATTAATTAATTAATTAATTAATTAATTA 1689
QY 301 CAACTACTGATCAATTTTCTCTCTGTCATGATTAATTAATTAATTAATTAATTAATTAAT 360
DB 1690 CAACTACTGATCAATTTTCTCTCTGTCATGATTAATTAATTAATTAATTAATTAATTAAT 1749
QY 361 TCTCCAAACCAAAACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 1750 TCTCCAAACCAAAACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1809
QY 421 TCTATCAAGAGCCAGTACCACTCATGATGAAGAAACACAGAGTACGAGAGGCTA 480
DB 1810 TCTATCAAGAGCCAGTACCACTCATGATGAAGAAACACAGAGTACGAGAGGCTA 1869
QY 481 AACTATCAAAACCACTACTCTTTCTCTACCTTATTTCTCAATCTTTTACCTTTTC 540
DB 1870 AACTATCAAAACCACTACTCTTTCTCTACCTTATTTCTCAATCTTTTACCTTTTC 1929
QY 541 CAAATCCCAATCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 600
DB 1930 CAAATCCCAATCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1989

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Oy	601	TATGTCGTAAAGAGATGGGGAGACCAACTCTGTATACTTCTGTAACAAGTTATA	660
Dd	1990	CATGTCGTAAAGAGATGGGGAGACCAACTCTGTATACTTCTGTACAAGTTATA	2049
Oy	661	CATGCTATCAAACCAGACTTGCTCCATAGTGAAGACTTGCTTTCAGAACATAGGGA	720
Dd	2050	CATGCTATCAAACCAGACTTGCTCCATAGTGGGGACTTGCTTTCAGAACATAGGGA	2109
Oy	721	TGAAGTAAGTGCCCGAAAAGTTGGGGAAAAAGTTCTTTCAAGAAGTTAAGTTATTT	780
Dd	2110	TGAAGTAAGTGCCCGAAAAGTTGGGGAAAAAGTTCTTTCAAGAAGTTAAGTTATTT	2169
Oy	781	AAT	840
Dd	2170	AAT	2229
Oy	841	TATGCGTGCTGTAGACACACACGCATACACATATATAGGAACATAGCCATTCTA	900
Dd	2230	TATGCGTGCTGTAGACACACACGCATACACATATATAGGAACATAGCCATTCTA	2289
Oy	901	AGAGCTGTATGCTTATGGAAGCTCTGACTAGGCATGATTTACGAAGGCMAAGTTGGCAT	960
Dd	2290	AGAGCTGTATGCTTATGGAAGCTCTGACTAGGCATGATTTGACGAAGGCMAAGTTGGCAT	2349
Oy	961	ATCATATGTATCTAAAAAAGCTGACATTCGACCCAGACATATATGTACTCTTTCTAAAAATTA	1020
Dd	2350	ATCATATGTATCTAAAAAAGCTGACATTCGACCCAGACATATATGTACTCTTTCTAAAAATTA	2409
Oy	1021	TAAATATATATCTAACAGAAAGAAAGAACCGTTGCTTGCATATCTACGCTAGTAGAGA	1080
Dd	2410	TAAATATATATCTAACAGAAAGAAAGAACCGTTGCTTGCATATCTACGCTAGTAGAGA	2469
Oy	1081	CTTTGAGGAAGAATTCAACAGTGCTCTTGACAGTGTTCAAGCCCAAGCAAGAAAGTTGA	1140
Dd	2470	CTTTGAGGAAGAATTCAACAGTGCTCTTGACAGTGTTCAAGCCCAAGCAAGAAAGTTGA	2529
Oy	1141	AGTTGCCTAGACAGAGAGACATTAAGTATCATGTCTCTTTAATCTAGCATACCCGGAAGTG	1200
Dd	2530	AGTTGCCTAGACAGAGAGACATTAAGTATCATGTCTCTTTAATCTAGCATACCCGGAAGTG	2589
Oy	1201	GAGAAAGGTGCGACAGGCTCAAGGCGTAATGTCATTCGCAATCAGCCCACTAAGTTGTCCT	1260
Dd	2590	GAGAAAGGTGCGACAGGCTCAAGGCGTAATGTCATTCGCAATCAGCCCACTAAGTTGTCCT	2649
Oy	1261	TTTCTGCTTGCTGTTCAACATGGAACATTTTGATTAAGTTAATFCTTCTATCTTGAAT	1320
Dd	2650	TTTCTGCTTGCTGTTCAACATGGAACATTTTGATTAAGTTAATFCTTCTATCTTGAAT	2709
Oy	1321	CTTCTAGAGAGTGTGACCAACTGACGTATGTTCCCTTGTGAAATTAATAACTGGTG	1380
Dd	2710	CTTCTAGAGAGTGTGACCAACTGACGTATGTTCCCTTGTGAAATTAATAACTGGTG	2769
Oy	1381	TTCTGCTTCATTA 1392	
Dd	2770	TTCTGCTTCATTA 2781	

XX	RESULT 11
ADQ38340	
ID	ADQ38340 standard; DNA; 2728 BP.
XX	
AC	
XX	
ADQ38340;	
XX	
DT	18-NOV-2004 (first entry)
XX	
DB	Human SNP containing myocardial infarction-associated gene, SEQ ID 3.
XX	
KM	Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM	cardiac; gene therapy; human; gene; de.
XX	
OS	Homo sapiens.
XX	

Pt	MW02004058052-A2.
Dd	15-JUL-2004 .
Xx	
Pf	22-DEC-2003; 2003WO-US040978 .
Xx	
Pf	20-DEC-2002; 2002US-0434778P .
Xx	
Pf	10-MAR-2003; 2003US-0453135P .
Xx	
Pf	30-APR-2003; 2003US-0466412P .
Xx	
Pf	23-SER-2003; 2003US-0504955P .
Xx	
Pa	(APPL-) APPLERA CORP.
Xx	
Pi	Cargill M., Devlin JI., Takubova O;
Dr	WI ; 2004-533949/51.
Xx	
DR	P-PSTB; ADQ39168.
Xx	
Pt	Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
Xx	
Ps	Claim 7; SEQ ID NO 3; 145pp; English.
Xx	
Cc	The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has constant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
Sq	Sequence 2728 BP; 798 A; 468 C; 450 G; 730 T; 0 U; 282 Other;
Query Match	80.6%; Score 1376.6; DB 13; Length 2728;
Best Local Similarity	99.8%; Pred. No. 2.Be-279;
Matches 1388; Conservative	1; Mismatches 0; Indels 2; Gaps 1;
Oy	1 AATGAAGATGCGATTTCACAGGTCAATCATTTGGAAATTAACAAGGCCTTCCAC 60 Db AAATAAATGATGATTTCCAGGTTAATTCATTGGAATTTAACAGGCCCTCACC 1399
Oy	61 TAAGAATCACCTTCCCATTCTTTTTTAGATTGTAATTAATATATACATTCATGATCCT 120 Db TTACTATACATCTTCCCCATCTTGTTAGATTGAATATATATACATTCATGATCCT 1459
Oy	121 TTTTCCTTTNACAGGGGGAATTTTCATATTTTACTGAGAAATTTGATTAAAAATGAA 180 Db TTATCATCATCTTCCAGGGGGAATTTTCATATTTTACTGAGCAAATTTGATTAAAATGAA 1519
Oy	1460 CCACGAGGAATTAATATNGTTTGAATAATATACAGTCACTTTCAAGGGCCAGCCTTGA 240 Cc ACCTAGAGGAATTAATATNGTTTGAATAATATACAGTCACTTTCAAGGGCCAGCCTTGA 1579

QY 241 CAAAATGTGAAGTTAAATTCCTCACTGTGCATCAAGATACATGTTGTTCCACATGAG 300
 DB 1580 CAAAATGTGAAGTTAAATTCCTCACTGTGCATCAAGATACATGTTGTTCCACATGAG 1639
 QY 301 CAACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 360
 DB 1640 CAACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1699
 QY 361 TCTCCACCAAAACATCAATGTTTATGTTCTGTATACAGATACAGATCTTGGTCTAC 420
 DB 1700 TCTCCACCAAAACATCAATGTTTATGTTCTGTATACAGATACAGATCTTGGTCTAC 1759
 QY 421 TCTATCAAGGCGCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 480
 DB 1760 TCTATCAAGGCGCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1819
 QY 481 AAACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 540
 DB 1820 AAACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1879
 QY 541 CAAATCCCAATCCCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 600
 DB 1880 CAAATCCCAATCCCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1939
 QY 601 CATGCTGTAAAGGAGATGGGAGATCACTCTGTTATACCTTGTATACAGATTATA 660
 DB 1940 CATGCTGTAAAGGAGATGGGAGATCACTCTGTTATACCTTGTATACAGATTATA 1999
 QY 661 CATGCTGTAAAGGAGATGGGAGATCACTCTGTTATACCTTGTATACAGATTATA 720
 DB 2000 CATGCTGTAAAGGAGATGGGAGATCACTCTGTTATACCTTGTATACAGATTATA 2059
 QY 721 TGAAGTAAAGTCCCTGAAGATTTGGGGGAAAGTTCTTTCAGAGATTAAATTATTT 780
 DB 2060 TGAAGTAAAGTCCCTGAAGATTTGGGGGAAAGTTCTTTCAGAGATTAAATTATTT 2149
 QY 781 AT 840
 DB 2120 AT 2177
 QY 841 TATGCTGTGTGTGACACACAGCATACACATATATATATATATATATATATATATATAT 900
 DB 2178 TATGCTGTGTGTGACACACAGCATACACATATATATATATATATATATATATATATAT 2237
 QY 901 AGAGCTGT 960
 DB 2238 AGAGCTGT 2297
 QY 961 ATCATTTGTAACTAAAAAGCTGACATTTGACCCAGACATATTTGATCTTTCTTAAAAATA 1020
 DB 2298 ATCATTTGTAACTAAAAAGCTGACATTTGACCCAGACATATTTGATCTTTCTTAAAAATA 2357
 QY 1021 TAAAT 1080
 DB 2358 TAAAT 2417
 QY 1081 CTTTGAAGAAATTTCAACAGTGTCTTCAAGAGTTTCAAGAGCCAAAGAAAGTTGA 1140
 DB 2418 CTTTGAAGAAATTTCAACAGTGTCTTCAAGAGTTTCAAGAGCCAAAGAAAGTTGA 2477
 QY 1141 AGTTGCTTAAGCCAGAGACAT 1200
 DB 2478 AGTTGCTTAAGCCAGAGACAT 2537
 QY 1201 GAGAGGCTGACAGAGCTCAAAAGGCTAAGTATTCATTCAGCAACATTAAGTTGCTT 1260
 DB 2538 GAGAGGCTGACAGAGCTCAAAAGGCTAAGTATTCATTCAGCAACATTAAGTTGCTT 2597
 QY 1261 TTTCTGTGTTTGTGTTCACCATGGAACATTTTATATATATATATATATATATATATATAT 1320
 DB 2598 TTTCTGTGTTTGTGTTCACCATGGAACATTTTATATATATATATATATATATATATATATAT 2657

QY 1321 CTTTGAAGAGTTCTGACCACTGACGATGTTTCCCTTTGTGAAATTAATAAATGCTG 1380
 DB 2658 CTTTGAAGAGTTCTGACCACTGACGATGTTTCCCTTTGTGAAATTAATAAATGCTG 2717
 QY 1381 TTTCTGTGTTTGTGTTCACCATGGAACATTTTATATATATATATATATATATATATAT 1440
 DB 2718 TTTCTGTGTTTGTGTTCACCATGGAACATTTTATATATATATATATATATATATATAT 2777
 RESULT 12
 ADQ38338
 ID ADQ38338 standard; DNA; 2771 BP.
 XX
 AC ADQ38338;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 1.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiac; gene therapy; human; gene; de.
 XX
 OS Homo sapiens.
 XX
 PN W0204058052-A2.
 PD
 XX 15-JUL-2004.
 PF 22-DEC-2003; 2003MO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JJ, Iakubova O;
 XX
 DR WPI; 2004-533949/51.
 DR P-PDSB; ADQ39166.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 7; SEQ ID NO 1; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiac activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC polynucleotide sequence represents a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This

CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiac activity.
 CC The nucleic acid of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC polynucleotide sequence represents a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

CC Sequence 2777 BP; 801 A; 489 C; 452 G; 754 T; 0 U; 281 Other;

CC Query Match 80.6%; Score 1376.6; DB 13; Length 2777;

CC Best Local Similarity 99.8%; Pred. No. 2.8e-279; Mismatches 1; Gaps 1;

CC Matches 1388; Conservative 1; Indels 2; Gaps 1;

CC 1 AATGAAGATGATGATTCAGAGTTAATTCATGGAATGAAATTAACAGGAGCCCTCTAC 60
 CC 1389 AATGAAGATGATGATTCAGAGTTAATTCATGGAATGAAATTAACAGGAGCCCTCTAC 1448
 CC 61 TAACTAATCACTTCCATCTTTTGTAGATTGAATATATATATATATATATATATAT 120
 CC 1449 TAACTAATCACTTCCATCTTTTGTAGATTGAATATATATATATATATATATATAT 1508
 CC 121 TTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGAAATTAAGAA 180
 CC 1509 TTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGAAATTAAGAA 1568
 CC 181 CCACTAGAGGAATTAATGTGTAGAAATTAACAGTATTTCTAAGGAGCCAGCTTGA 240
 CC 1569 CCACTAGAGGAATTAATGTGTAGAAATTAACAGTATTTCTAAGGAGCCAGCTTGA 1628
 CC 241 CAAATTTGTGAAGTTAATTTCTCACTGTCTGTCATGAGATCTATGTTTCCACTATG 300
 CC 1629 CAAATTTGTGAAGTTAATTTCTCACTGTCTGTCATGAGATCTATGTTTCCACTATG 1688
 CC 301 CAACTAATCACTTCCATCTTTTGTAGATTGAATATATATATATATATATATATAT 360
 CC 1689 CAACTAATCACTTCCATCTTTTGTAGATTGAATATATATATATATATATATATAT 1748
 CC 361 TTTTCAACCAAAACATCATATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
 CC 1749 TTTTCAACCAAAACATCATATTTATTTATTTATTTATTTATTTATTTATTTATTT 1808
 CC 421 TTTTCAACCAAGGAGTATCACTCATGTAAGAAACACAGAGTATGAGAGGCTA 480
 CC 1809 TTTTCAACCAAGGAGTATCACTCATGTAAGAAACACAGAGTATGAGAGGCTA 1868
 CC 481 AATCTCATCAAAACACATCATGTTTCTCTTACCTTATCTCAATCTTTTACCTTTT 540
 CC 1869 AATCTCATCAAAACACATCATGTTTCTCTTACCTTATCTCAATCTTTTACCTTTT 1928
 CC 541 CAAATCCCAATCCCAATCATGTTTCTCTTCTTATCTCCCTCTCTCCCTTTTACCTTC 600
 CC 1929 CAAATCCCAATCCCAATCATGTTTCTCTTCTTATCTCCCTCTCTCCCTTTTACCTTC 1988

CC 601 CATGCTCTTAAGAGAGATGGGAGCATCTCTGTTATATCTTCTATACAGTTATA 660
 CC 1989 CATGCTCTTAAGAGAGATGGGAGCATCTCTGTTATATCTTCTATACAGTTATA 2048
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 CC 2049 CATGCTCTTAAGAGAGATGGGAGCATCTCTGTTATATCTTCTATACAGTTATA 2108
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 CC 781 AT 840
 CC 2169 AT 2226
 CC 841 TATGCTGTGTGTAGACACACCATATACATATATATATATATATATATATATATAT 900
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 CC 2287 AGAGCTGTATGTGTATGAGAGTCTGACTAGGATGATTTTACAGAGGCAAGATTGCA 2346
 CC 961 ATCATTTTAATTAATAAAGCTGACATTTGACATGACCAATATTTTCTTTTAAATTA 1020
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 CC 1021 TAAAT 1080
 CC 2407 TAAAT 2466
 CC 1081 CTTTGAAGAGAAATTAACAGTGTCTTACAGAGTCTTACAGAGGCAAGAGTTGA 1140
 CC 2467 CTTTGAAGAGAAATTAACAGTGTCTTACAGAGTCTTACAGAGGCAAGAGTTGA 2526
 CC 1141 AGTTGCTTAACCAAGAGACATATATATATATATATATATATATATATATATATAT 1200
 CC 2527 AGTTGCTTAACCAAGAGACATATATATATATATATATATATATATATATATATAT 2586
 CC 1201 GAGAGAGGTCAGAGGCTCAAAAGGCAATTAAGTCAATTCAGAGCAATTAAGTTCCT 1260
 CC 2587 GAGAGAGGTCAGAGGCTCAAAAGGCAATTAAGTCAATTCAGAGCAATTAAGTTCCT 2646
 CC 1261 TTTCTGTTTCTGTTTCAACATGGAACATTTTATATATATATATATATATATATAT 1320
 CC 2647 TTTCTGTTTCTGTTTCAACATGGAACATTTTATATATATATATATATATATATAT 2706
 CC 1321 CTTCTAGAGAGTGTCTGACCACTGAGATATTTTCTTGTGAATTAATACTGGTG 1380
 CC 2707 CTTCTAGAGAGTGTCTGACCACTGAGATATTTTCTTGTGAATTAATACTGGTG 2766
 CC 1381 TTCGTGTTTCAAT 1391
 CC 2767 TTCGTGTTTCAAT 2777

CC RESULT 14
 CC ADQ38341
 CC ID ADQ38341 standard; DNA; 2831 BP.
 CC AC ADQ38341;
 CC DT 18-NOV-2004 (First entry)
 CC XX Human SNP containing myocardial infarction-associated gene, SBO ID 4.
 CC DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 CC KW cardiant; gene therapy; human; gene; de.
 CC OS Homo sapiens.
 CC XX
 CC XX
 CC PN MO2004058052-A2.

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Qy	1261	TTTCTGCTTTCGATTCACATGGAACAATTGATTAAGTTAAATCCTCTATCTTGAAT	1320
Db	2630	TTTCTGCTTTCGATTCACATGGAACAATTGATTAAGTTAAATCCTCTATCTTGAAT	2689
Qy	1321	CTTCTAGAGAGTTGCTGACCACTGACGTATGTTCCCTTTGGAATTAATAAATCTGCTG	1380
Db	2690	CTTCTAGAGAGTTGCTGACCACTGACGTATGTTCCCTTTGGAATTAATAAATCTGCTG	2749
Qy	1381	TTCTGGTTC	1389
Db	2750	TTCTGGTTC	2758

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GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model

Run on: April 18, 2006, 12:18:29 ; Search time 8289.18 Seconds

(without alignments)
9634.919 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_esc1.*
2: gb_esc2.*
3: gb_esc3.*
4: gb_esc4.*
5: gb_esc5.*
6: gb_esc6.*
7: gb_esc7.*
8: gb_esc8.*
9: gb_esc9.*
10: gb_esc10.*
11: gb_esc11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	802	47.0	943	5 BX405727	BX405727 BX405727
C 2	527.2	30.9	532	6 CH156936	CH156936 K-EST0215
C 3	486.6	28.5	515	5 BX414387	BX414387 BX414387
C 4	451.2	26.4	524	7 CO775183	CO775183 ILLUMIN
C 5	446	26.1	518	9 AQ456663	AQ456663 HS 5166 A
C 6	373	21.9	373	1 AV647038	AV647038 AV647038
C 7	373	21.9	374	1 AV647182	AV647182 AV647182
C 8	321	18.8	385	1 AV656454	AV656454 AV656454
C 9	236.8	13.9	721	1 AM018125	AM018125 AM018125
C 10	163.6	9.6	583	7 CO740602	CO740602 SILL07a27
C 11	149.6	8.8	374	6 CP106639	CP106639 ZP0904D3
C 12	149.6	8.8	688	5 BX926315	BX926315 BX926315
C 13	149.6	8.8	690	5 BX925779	BX925779 BX925779
C 14	147	8.6	257	7 CO775581	CO775581 ILLUMIN
C 15	142.4	8.3	400	7 CO701325	CO701325 DG32-1f6
C 16	138.2	8.1	592	10 AM018944	AM018944 AM018944
C 17	122.4	7.2	592	10 CE730574	CE730574 LIGT-988-
C 18	119.6	7.0	744	1 AM019095	AM019095 AM019095
C 19	118.2	6.9	835	1 AM015797	AM015797 AM015797
C 20	118.2	6.9	816	6 CA456053	CA456053 AGENCOURT
C 21	113.8	6.7	799	1 AM014733	AM014733 AM014733
C 22	107.4	6.3	574	3 BP104057	BP104057 BP104057

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C 24	91.6	5.4	533	3 BP103684	BP103684 BP103684
C 25	86.6	5.1	555	5 BX514685	BX514685 BX514685
C 26	86.2	5.0	363	5 BU182460	BU182460 AGENCOURT
C 27	86.2	5.0	698	9 AQ741865	AQ741865 HS 5568 B
C 28	84.4	4.9	681	10 AG115419	AG115419 Pan trogl
C 29	84.2	4.9	647	10 AG017260	AG017260 Homo sapl
C 30	84	4.9	233	9 AQ426652	AQ426652 CTIB1-B1-
C 31	83.8	4.9	454	3 BP101424	BP101424 BP101424
C 32	83.4	4.9	310	1 AL603386	AL603386 DKFZP686D
C 33	83.4	4.9	366	1 AL603402	AL603402 DKFZP686E
C 34	83.4	4.9	763	1 B2610396	B2610396 WMAA81TR
C 35	83.4	4.9	511	9 BZ612790	BZ612790 WMAA51STP
C 36	83	4.9	705	10 AG151432	AG151432 Pan trogl
C 37	82.8	4.9	318	6 CD242472	CD242472 AGENCOURT
C 38	82.6	4.8	310	1 AM407679	AM407679 UI-HF-BMO
C 39	82.6	4.8	396	1 AA569240	AA569240 nm1b04.8
C 40	82.4	4.8	528	3 AQ211789	AQ211789 HS 3234 B
C 41	81.8	4.8	389	3 BP102450	BP102450 BP102450
C 42	81.6	4.8	477	8 DR033758	DR033758 5000DCB12
C 43	81.2	4.8	409	9 B55158	B55158 CIT-HSP-386
C 44	81.2	4.8	602	9 AQ488141	AQ488141 RPCI-11-2
C 45	81.2	4.8	840	8 CX871715	CX871715 H8SC4_60

ALIGNMENTS

RESULT 1
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LOCUS BX405727 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
DEFINITION CS0DM008Y108 3-PRIME, mRNA sequence.
ACCESSION BX405727
VERSION BX405727.2 GI:46924492

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 943)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30635411.

CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 10715.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DM008B04NP1c=10715.f.

FEATURES
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ORIGIN

QY	565	TTTCTCTTCTTACCTCCCTCTCCCTTTACCTCCATGGCTCTTAAGAAGATGGG	624
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LOCUS			
DEFINITION			
BX414387 Homo sapiens FETAL LIVER Homo sapiens cDNA clone			
CSGDM008Y108 3-PRIME, mRNA sequence.			
ACCESSION			
BX414387			
VERSION			
BX414387.2 GI:46928493			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
Organism			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Homnidae; Homo.			
1 (bases 1 to 515)			
Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
COMMENT			
On May 13, 2003 this sequence version replaced gi:30645720.			
REFERENCE			
AUTHORS			
TITL			
JOURNAL			
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/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA			
was primed with a NotI-oligo (dT) primer. Five prime end			
enriched, double-strand cDNA was digested with Not I and			
cloned into the Not I and EcoRV sites of the pCMVSPORT 6			
vector. Library was not normalized."			
ORIGIN			
Query Match			
Best Local Similarity 99.0%; Score 486.6; DB 5; Length 515;			
Matches 489; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
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Db	515	TTCACACATATATATGAAAGCAATTAAGCAATCTTAAGACCTTGATGTTATGAGAGCTTG	456
QY	927	ACTAGGCATGATTTTACAGAGCAAGATTTGGATATCATTTGATTAATATAAAGCTGACAT	986
Db	455	ACTAGGCATGATTTTACAGAGCAAGATTTGGATATCATTTGATTAATATAAAGCTGACAT	396
QY	987	TGACCAAGCATATTTGTAATCTTTCTTAATAATATATATATATATGCTAACGAAGAAGA	1046
Db	395	TGACCAAGCATATTTGTAATCTTTCTTAATAATATATATATATATGCTAACGAAGAAGA	336
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Db	335	GAACCGTTCGTTTGCAATCTACAGCTAGTAGAGCTTTGAGGAAGAATTCAAAGCTGTGT	276
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Db	275	CTTCAGCAGAGTGTTCAGAGCCAAAGCAGAAGTTGAAGTTGCTCTAAGCCAGAGGAATNTAAGT	216
QY	1167.	ATCATGTCTCCTTTAATAGATATACCCGGAAGTGGAGAAGGGTGCACAGGCTCAAAAGC	1226
Db	215	ATCATGTCTCCTTTAATAGATATACCCGGAAGTGGAGAAGGGTGCACAGGCTCAAAAGC	156
QY	1227	ATAAGCATATTCCAATCAGCCAACTAAGTTGTCTTTTCTGTGTTTCGTGTTCAACATGGA	1286
Db	155	ATAAGCATATTCCAATCAGCCAACTAAGTTGTCTTTTCTGTGTTTCGTGTTCAACATGGA	96
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QY	1347	CGTAGGTTCCTTT	1360
Db	35	CGTAGGTTCCTTT	22

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LOCUS	
DEFINITION	C0775183 MCO_52421 Katze MNV Macaca nemestrina cDNA clone
	ILUMNGEN:28458 5' similar to Bases 5 to 424 highly similar to human P9
	(hs.1130), mRNA sequence.

ACCESSION	CO775183	GI:50976446
VERSION	CO775183.1	
KEYWORDS	EST	
SOURCE	Macaca nemestrina (pig-tailed macaque)	
ORGANISM	Macaca nemestrina	

REFERENCE
AUTHORS

Magness, C. L., Pellin, P. C., Thomas, M. J., Korth, M. J., Agy, M. B.,
1 (bases 1 to 524) Magnan, D. G., Korte, M. G. and
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

TITLE	JOURNAL	COMMENT
Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human	Genome Biol. 6 (7), R60 (2005)	
Contact: C. Magness	15598449	

illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.21. 661 Q20 bases. Library Preparation: Prof.
Michael Katze lab at University of Washington DNA Sequencing:
illumigen Biosciences Inc. For further information, see
<http://www.macaque.org>
PCR Primers
FORWARD: CCCCTACCTAAAGGACAAAA
BACKWARD: CACTATAGGGCGCAATGGGA
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POLYA=Yes.

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KEYWORDS
EST.
Homo sapiens (human)

SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 (bases 1 to 373)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL
PUBMED
11752456

COMMENT
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel.: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
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Location/Qualifiers
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Matches 373; Conservative 0; Mismatches 0;

118 GCTTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGATTAGAAATG 177
1 GCTTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGATTAGAAATG 60

178 GAACCACTAGAGAAATATATATGTGTAGAAATTAACATCTTTAAAGGCCCAAGCCT 237
61 GAACCACTAGAGAAATATATATGTGTAGAAATTAACATCTTTAAAGGCCCAAGCCT 120

238 TGACAAATTTGAAATTAATTTCTCCATCTGTCCATCAATTAATGTTTCCCACTA 297
121 TGACAAATTTGAAATTAATTTCTCCATCTGTCCATCAATTAATGTTTCCCACTA 180

298 TGGCAACTACTCACTCAATTTTCCCTCTTACAGAGATTCATCTTCCGATCTTCTT 357
181 TGGCAACTACTCACTCAATTTTCCCTCTTACAGAGATTCATCTTCCGATCTTCTT 240

358 GCTTCTCCACCAAAACATCATGTTTATTAAGTTCTGTATACAGTACAGATCTTTGGTC 417
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301 TACTCTATCAAGAGCCAGTACCACTCATGAGAAAGAACACAGAGTAGCTGAGAGG 360

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LOCUS
AV647182 374 bp mRNA linear EST 15-JAN-2002
DEFINITION
AV647182 GLC Homo sapiens cDNA clone GLCAVF01 3, mRNA sequence.
ACCESSION
AV647182
VERSION
AV647182.1 GI:9868196

KEYWORDS
EST.
Homo sapiens (human)

SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 (bases 1 to 374)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL
PUBMED
11752456

COMMENT
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel.: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.2e-70; Indels 0; Gaps 0;
Matches 373; Conservative 0; Mismatches 0;

118 GCTTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGATTAGAAATG 177
1 GCTTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTGATTAGAAATG 60

178 GAACCACTAGAGAAATATATATGTGTAGAAATTAACATCTTTAAAGGCCCAAGCCT 237
61 GAACCACTAGAGAAATATATATGTGTAGAAATTAACATCTTTAAAGGCCCAAGCCT 120

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121 TGACAAATTTGAAATTAATTTCTCCATCTGTCCATCAATTAATGTTTCCCACTA 180

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181 TGGCAACTACTCACTCAATTTTCCCTCTTACAGAGATTCATCTTCCGATCTTCTT 240

358 GCTTCTCCACCAAAACATCATGTTTATTAAGTTCTGTATACAGTACAGATCTTTGGTC 417
241 GCTTCTCCACCAAAACATCATGTTTATTAAGTTCTGTATACAGTACAGATCTTTGGTC 300

418 TACTCTATCAAGAGCCAGTACCACTCATGAGAAAGAACACAGAGTAGCTGAGAGG 477
301 TACTCTATCAAGAGCCAGTACCACTCATGAGAAAGAACACAGAGTAGCTGAGAGG 360

478 CTAATACTCATCA 490
361 CTAATACTCATCA 373

RESULT 8
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LOCUS AV656454 GLC Homo sapiens cDNA clone GLCERB05 3', mRNA sequence.
DEFINITION AV656454
ACCESSION AV656454
VERSION AV656454.1 GI:9877468
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Shen, K., Lu, G., Pu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
JOURNAL Contact: Zeguang Han
PUBMED Chinese National Human Genome Center at Shanghai
COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
location/Qualifiers
1. 385
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCERB05"
/issue="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 18.8%; Score 321; DB 1; Length 385;
Best Local Similarity 87.7%; Pred. No. 4.5e-59;
Matches 385; Conservative 0; Mismatches 0; Indels 54; Gaps 1;
QY 933 CATGATTTCAGAGGAGGAGATGGCATATCATTTGTAATACTAATAAAGCTGACATTCGCC 992
DB 1 CATGATTTCAGAGGAGGAGATGGCATATCATTTGTAATACTAATAAAGCTGACATTCGCC 60
QY 993 AGACATATTTGTAATCTTTCTTAATAATAATAATAATAATAATAATAATAATAATAATA 1052
DB 61 AGACATATTTGTAATCTTTCTTAATAATAATAATAATAATAATAATAATAATAATAATA 77
QY 1053 TTGGTTGCAATCAAGTAGTAGAGACTTTGAGAGAAATTCACAGAGTGTCTTCAG 1112
DB 78 -----TTCAGCTAGTAGTAGAGACTTTGAGAGAAATTCACAGAGTGTCTTCAG 126
QY 1113 CAGTGTTCAGAGCCAGAGCAAGAAAGTTGAAGTTCCTAGACCAGAGGACATTAAGTATCATG 1172
DB 127 CAGTGTTCAGAGCCAGAGCAAGAAAGTTGAAGTTCCTAGACCAGAGGACATTAAGTATCATG 186
QY 1173 TTCCTTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1232
DB 187 TTCCTTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 246
QY 1233 CATTCGAATCAGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1292
DB 247 CATTCGAATCAGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 306

RESULT 9
AM018125/c 721 bp mRNA linear EST 29-JUN-2005
LOCUS AM018125 KN-252-liver, Bos taurus Bos taurus cDNA clone C0007416a18
DEFINITION AM018125
ACCESSION AM018125
VERSION AM018125.1 GI:68319317
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 721)
Anderson, S.I., Taylor, R., Talbot, R., Speed, D., Law, A.S., Humphray, S., Hanotte, O., Mwakaya, J., and Archibald, A.L.
Development of cDNA and EST resources for studying host responses to trypanosome infection in cattle
Unpublished (2005)
JOURNAL Contact: Anderson SI
COMMENT Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM.
location/Qualifiers
1. 721
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="C0007416a18"
/issue type="liver"
/clone_lib="KN-252-liver, Bos taurus"
/note="Breed: N'dama"

ORIGIN
Query Match 13.9%; Score 236.8; DB 1; Length 721;
Best Local Similarity 67.9%; Pred. No. 9.6e-41;
Matches 429; Conservative 0; Mismatches 177; Indels 26; Gaps 6;
QY 1 AATGAAGATGATTTTCCAGG-TTAATTCATTTGGAATTTGAATAATTAACAGGCTCTCA 59
DB 629 AATGAAGATGATTTTCCAGG-TTAATTCATTTGGAATTTGAATAATTAACAGGCTCTTA 570
QY 60 CTAACTAATCACTTCCATCTTTGTTAGATTTGAATTAATTAATTAATTAATTAATTAATTA 119
DB 569 CTAACTAATCACTTCCATCTTTGTTAGATTTGAATTAATTAATTAATTAATTAATTA 512
QY 120 TTTTCTCTTTACAGGGAGA-----ATTGATATTTTACCTGAGCAATTAAT 169
DB 511 TTTTCTCTTTTATGGGAGAAAGTTAGTAGACTTCAATTTTCTTGAATTAATTAATTA 452
QY 170 AGAAATGGAACACATAGAGAAATTAATGTTAGGAATTAATTAATTAATTAATTAATTA 229
DB 451 AGAAATGGAACACATAGAGAAATTAATGTTAGGAATTAATTAATTAATTAATTAATTA 392
QY 230 CCAGCCTTGAACAAATTTGAAGTTAAATTTCTCACTGTGTCAATCAGATACTAATGTT 289
DB 391 CCAGCCTTGAACAAATTTGAAGTTAAATTTCTCACTGTGTCAATCAGATACTAATGTT 332
QY 290 CTCACATATGGAACATTAATCTCAATTTTCTCTCTTGAAGAGATTCATTTCCGA 349
DB 331 TTCACAGGGAGCACTACT-----GTTTTTTTGTCTTGAAGAGATTCATTCACAGCA 277
QY 350 TCTTCTTGTCTTCAACCAAAACATCAATGTTAATTAATTAATTAATTAATTAATTAAT 409

Db 276 TTTTAAACATCCCCCAAGTAAATTAATGATTTGT-----ATCAGAGAT 224
 Qy 410 CTTTGCTACTATACAGAGCCAGTACCACTATGAAGAAACAGAGATAG 469
 Db 223 ACTGATTAATCATTAAGGCGAGCCCAATTCATGAGAAACAGAGAGAG 164
 Qy 470 CTGAGAGCTAAAGTCAAAAACACTACTCTCTCTCTA-CCTATTCTCAATC 528
 Db 163 GTGAGAGTAAAGTCAAGGAGACACTACTTTTTCATATCTTATTCCTGATC 104
 Qy 529 TTTTACCTTTTCGAATCCCAATCCCAATCAGTTTTCCTTTTACTCTCTCTC 588
 Db 103 CTTTATCTTTTCAACCTCTTAATGCCCAATCATTTTTTTTTTTCCCTTTTCCC 44
 Qy 589 CTTTAACTTCATGCTGCTTAAAGAGAGA 620
 Db 43 TACATAGGCATTAAGGGGAGAGAGAGAAAAA 12

RESULT 10
 CO740602 583 bp mRNA linear EST 29-JUL-2004
 LOCUS S1107a27101e1 squirrel liver library 3 Spermophilus lateralis cDNA
 DEFINITION clone 27101 5', mRNA sequence.
 ACCESSION CO740602
 VERSION CO740602.1 GI:50827872
 KEYWORDS EST.
 SOURCE Spermophilus lateralis (golden-mantled ground squirrel)
 ORGANISM Spermophilus lateralis
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Buteria; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Sclerogomphii; Sclerogomphii; Sclerogomphii; Sclerogomphii; Sclerogomphii;
 Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
 Rogers, J., and Cossins, A.R.
 Microarray analysis of transcriptional changes during hibernation
 in the golden mantled ground squirrel, Spermophilus lateralis
 unpublished (2004)
 CONTACT: Andrew R. Cossins
 Laboratory for Environmental Gene Regulation
 University of Liverpool
 School of Biological Sciences, The Biosciences Building, Crown
 Street, Liverpool, United Kingdom, L69 7ZB
 Tel: +44(0)151-795-4510
 Fax: +44(0)151-795-4431
 Email: cossins@liverpool.ac.uk
 Vector has been trimmed from this EST.
 Plate: 27 row: 1 column: 01
 Seq primer: TTTTATG 5' LD (5'-CTGGGAGAGCGGCATGTTGTTGCT-3')
 High quality sequence stop: 583.
 Location/Qualifiers

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 /dev_stage="Adult"
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 /clone_1ib="squirrel liver library 3"
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 Site 2: 5' LD GGCATTAAGGCGC; Normalized cDNA library
 prepared from liver of hibernating and summer animals"

ORIGIN
 Query Match 9.6%; Score 163.6; DB 7; Length 583;
 Best Local Similarity 67.9%; Pred. No. 8.1e-25;
 Matches 326; Conservative 0; Mismatches 129; Indels 25; Gaps 6;
 911 TGGTATGAGGCTGATGAGCATGATTTTCAAGAGGAGATGGCATATCATTTGA 970

Db 120 TGATTATGCACTCTGCTGGGAATGTTCCATCAGGAGGCTG---CAGTCACTTA 176
 Qy 971 CTAAGAAAGTACATTAAGCCAGACATATTTGATCTTTCTTAAATATATATATAT 1030
 Db 177 CTAAGAAAGTACATTAAGGAGATTTATCCCTGCTGAGAAAAATATATCTTAC 236
 Qy 1031 CTTAAGAAAGGAGACCGCTTCTGTTGCAATCTAAGCTATGAGACCTTTAGGA 1090
 Db 237 AGAA-----AGAACTATCCCATTTGACCAAGCAATCTAGAGATTTCTTAAGGA 285
 Qy 1091 GAATTAACAGTGTGCTTGAAGTCTGAGAGTCTGAGCAAGCAAGATTTGAAGTCCTAG 1150
 Db 286 GAATTAACAGATATATCTTCAACATTAATCTGAGTCAAGCA-----GAAGTCTTAG 339
 Qy 1151 ACCAGAGCAATTAATATATATCTCTTAACTAGATACCCGAGATGAGAGAGGTTG 1210
 Db 340 ACCAGAGCAATTAATATATCTCTTAACTAGATACCCGAGATGAGAGAGGTTG 1210
 Qy 1211 CAGCAGGCTCAAGGATTAATGATATATATATATATATATATATATATATATAT 1269
 Db 397 CA-CAGGCTCAAGGCTGAGTCAATTAACCAAGTAACTATATATATATATATATAT 455
 Qy 1270 TCGTGTACAGTGAACATTTGATTAATATATATATATATATATATATATATATAT 1329
 Db 456 CAGTGTACAGGATTAATGATATATATATATATATATATATATATATATATATATAT 515
 Qy 1330 AGTGTCTGACCACTGAGTATGTTCCCTTGTGATTAATTAATGCTGTCTGCTTC 1389
 Db 516 GGTCTGACCACTGAGTATGTTCCCTTGTGATTAATTAATGCTGTCTGCTTC 575

RESULT 11
 CF106639 374 bp mRNA linear EST 22-JUL-2003
 LOCUS ZP0904D3 Pig liver cDNA Sus scrofa cDNA clone 04D3 similar to
 DEFINITION Coagulation Factor IX (F9), mRNA sequence.
 ACCESSION CF106639
 VERSION CF106639.1 GI:33145706
 KEYWORDS EST.
 SOURCE Sus scrofa
 ORGANISM Sus scrofa (pig)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1 (bases 1 to 374)
 Ernest, C.W., Raney, N.E., Martinez, M.M., Hargrave, K.M., Hill, G.M. and
 Link, J.B.
 Identification of differentially expressed genes in pig liver

FEATURES
 source
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 /organism="Sus scrofa"
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 /db_xref="taxon:9823"
 /clone="04D3"
 /clone_1ib="Pig liver cDNA"
 Location/Qualifiers

ORIGIN
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 811 TGGTATGAGGCTGATGAGCATGATTTTCAAGAGGAGATGGCATATCATTTGA 970

RESULT 5
 US-09-949-016-5252
 ; Sequence 5252; Application US/09949016
 ; Patent No. 681339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5252
 ; LENGTH: 2833
 ;
 ; TYPE: DNA
 ;
 ; ORGANISM: Human
 ;
 US-09-949-016-5252

[illegible]

|||||
Db 2662 TTTCGTTTCGTTTCACCAATGGAATTTGATTAATTAATTCCTGATCTGAT 2721
Qy 1321 CTCTAGAGAGTTCTGACCACTGACGATGATTTCCCTTTGTAATTAATAAATCTGTG 1380
Db 2722 CTCTAGAGAGTTCTGACCACTGACGATGATTTCCCTTTGTAATTAATAAATCTGTG 2781
Qy 1381 TTCTGTTTCAT 1391
Db 2782 TTCTGTTTCAT 2792

RESULT 7
US-08-742-877-1
Sequence 1, Application US/08742877
Patent No. 6046380
GENERAL INFORMATION:
APPLICANT: CLARK, Anthony J.
TITLE OF INVENTION: DNA SEQUENCES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,877
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9408717.8
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: FLESHNER, RAZ B.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0623, 0470001/REF
TELEPHONE: (202) 371-2500
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2802 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
FEATURES:
NAME/KEY: CDS
LOCATION: 30..1412
NAME/KEY: sig_peptide
LOCATION: 30..167
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 168..1412
US-08-742-877-1

Query Match. 81.2%; Score 1385.8; DB 3; Length 2802;
Best Local Similarity 68.2%; Pred. No. 0;
Matches 947; Conservative 440; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATGAGAAGATTTCCAGGTTAATTCAATGGAATGAATAAAGAGGCTCTAC 60
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Qy 61 TAACTAATCACTTCCATCTTTGTTGATTTGAATTAATATACATTCATGATCTTCT 120

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Db 1474 UAACTAATCACTTCCATCTTTGTTGATTTGAATTAATATACATTCATGATCTTCT 1533
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Qy 421 TCTATCAAGGCGGCACTGACCTGATGAGAAATTAAGTCTTCCGATCTTCTGCT 480
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Qy 481 AAATCTAATCACTCAATTTTCCCTCTGAGCAATTTCTGAGCAATTTCTGAGCAATTTCTGAG 540
Db 1894 AAATCTAATCACTCAATTTTCCCTCTGAGCAATTTCTGAGCAATTTCTGAGCAATTTCTGAG 1953
Qy 541 CAAATCCCAATCCCAATGATTTTCTCTTCTTCTGATGAGCAATTTCTGAGCAATTTCTGAG 600
Db 1954 CAAATCCCAATCCCAATGATTTTCTCTTCTTCTGATGAGCAATTTCTGAGCAATTTCTGAG 2013
Qy 601 CATGTTGTTAAGGAGATGAGGAGCAATTTCTGATGAGCAATTTCTGAGCAATTTCTGAG 660
Db 2014 CATGTTGTTAAGGAGATGAGGAGCAATTTCTGATGAGCAATTTCTGAGCAATTTCTGAG 2073
Qy 661 CATGTTGTTAAGGAGATGAGGAGCAATTTCTGATGAGCAATTTCTGAGCAATTTCTGAG 720
Db 2074 CATGTTGTTAAGGAGATGAGGAGCAATTTCTGATGAGCAATTTCTGAGCAATTTCTGAG 2133
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Db 2434 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2493
Qy 1081 CTTGAGGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140
Db 2494 CTTGAGGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2553
Qy 1141 AGTTGCTTAATCAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200

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Db 2614 GAGAGAGGTGAGCAGGCTCAAGAGCAATAGTCAATCCATCAGCCAACTAAGTTGCT 2673
Qy 1261 TTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 1320
Db 2674 TTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 2733
Qy 1321 CTTCTAGAGAGGTGAGCAGGCTCAAGAGCAATAGTCAATCCATCAGCCAACTAAGTTGCT 1380
Db 2734 CTTCTAGAGAGGTGAGCAGGCTCAAGAGCAATAGTCAATCCATCAGCCAACTAAGTTGCT 2793
Qy 1381 TTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 1389
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RESULT 8
US-09-328-925-3
; Sequence 3, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328, 925
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-3

Query Match 74.6%; Score 1273; DB 3; Length 1273;
Best Local Similarity 100.0%; Pred. No. 1,6e-308;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GGGCTCTCACTAATCACTTCCGACTTTTGTAGTGAATATATATATATATATATATATAT 110
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Qy 111 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTTATATTTTACCTGAGCAAAATGATTA 170
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Qy 171 GAAATGGAACCACTAGAGAAATATATATATATATATATATATATATATATATATATAT 230
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Qy 411 TTTGCTCTCTATATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 470
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Db 421 TGAAGGCTTAAATCAATCAAAATCACTAATCTTCTTCTTCTTCTTCTTCTTCTTCTT 480
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Db 481 TTAACCTTTTCAATCCCAATCCCAATCAATTTTCTTTCTTCTTCTTCTTCTTCTTCTT 540
Qy 591 TTTTACCTTCCATGCTGCTTAAAGAGAGATGAGGAGCAATCTGCTTAACTCTGTA 650
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Qy 771 AAGTTATTTATATATATATATATATATATATATATATATATATATATATATATATAT 830
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Qy 951 AGATTGCAATATATATATATATATATATATATATATATATATATATATATATATATAT 1010
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Db 961 CTAAATATATATATATATATATATATATATATATATATATATATATATATATATAT 1020
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Db 1081 AAGAGTTGAGTGTGCTTGAACAGAGGACATATATATATATATATATATATATATATAT 1140
Qy 1191 CCCCAGAGTGAAGAGGAGTGAAGAGGCTCAAGGCAATATATATATATATATATATATAT 1250
Db 1141 CCCCAGAGTGAAGAGGAGTGAAGAGGCTCAAGGCAATATATATATATATATATATATAT 1200
Qy 1251 AAGTTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCT 1310
Db 1201 AAGTTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCT 1260
Qy 1311 TATCTTGAATCTT 1323
Db 1261 TATCTTGAATCTT 1273

RESULT 9
US-09-328-925-83
; Sequence 83, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328, 925
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0

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QY 351 CTTCTTTCCTTCCCAACCAAAACATCAATGTTTATAGTTCGTATACAGTACAGATC 410
Db 301 CTTCTTTCCTTCCCAACCAAAACATCAATGTTTATAGTTCGTATACAGTACAGATC 360
QY 411 TTTGTCTACTCTATCAAGAGCCAGTACCACTCATGAAAGAAACACAGAGTACG 470
Db 361 TTTGTCTACTCTATCAAGAGCCAGTACCACTCATGAAAGAAACACAGAGTACG 420
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Db 481 TTACCTTTTCCAAATCCCAATCCCAATCAATTTTCTCTTCTTCTTCTCTCTCC 540
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Db 541 TTTTACCTTCCATGCTGTTTAAAGAGAGATGGAGATCAATCTGTATATCTTCTGA 600
QY 651 CACAGTTATACATGCTATCAAAACCAAGCTTCTCATAGTGAAGATCTTCTTCTAG 710
Db 601 CACAGTTATACATGCTATCAAAACCAAGCTTCTCATAGTGAAGATCTTCTTCTAG 660
QY 711 AACATAGGATGAAGTAAAGTCTGCTGAAAGTTTGGGGGAAAGTTTCTTCTGAGAGTT 770
Db 661 AACATAGGATGAAGTAAAGTCTGCTGAAAGTTTGGGGGAAAGTTTCTTCTGAGAGTT 720
QY 771 AAGTATTTTAG 830
Db 721 AAGTATTTTAG 780
QY 831 TGTGTGTGTATGTCGT 890
Db 781 TGTGTGTGTATGTCGT 840
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Db 901 AGATTGCAATCTATCTTAACTAAAGCTGACATTTGACCCAGACATATTTGTATCTTT 960
QY 1011 CTAAATAATAG 1070
Db 961 CTAAATAATAG 1020
QY 1071 CTAGTAAAGCTTGAAGAGAAATTTCAACAGTGTCTTCAAGAGTGTGAGAGCCAGC 1130
Db 1021 CTAGTAAAGCTTGAAGAGAAATTTCAACAGTGTCTTCAAGAGTGTGAGAGCCAGC 1080
QY 1131 AAGAAAGTGAAGTGTCTAGACCAAGACATATAGTATCAATGTCCTTAACTAGATAT 1190
Db 1081 AAGAAAGTGAAGTGTCTAGACCAAGACATATAGTATCAATGTCCTTAACTAGATAT 1140
QY 1191 CCCCAGAGTGAAGAGGCTGACAGAGCTCAAGGCTAAAGCTAAATTCATTCAGAGCACT 1250
Db 1141 CCCCAGAGTGAAGAGGCTGACAGAGCTCAAGGCTAAAGCTAAATTCATTCAGAGCACT 1200
QY 1251 AAGTGTCTCTTCTGT 1310
Db 1201 AAGTGTCTCTTCTGT 1260
QY 1311 TATCTTGAATCTT 1323
Db 1261 TATCTTGAATCTT 1273

RESULT 11
US-09-328-925-77
; Sequence 77, Application US/09328925

Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-77
Query Match 74.5%; Score 1271.4; DB 3; Length 1273;
Best Local Similarity 99.9%; Pred. No. 4.1e-308;
Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 51 GGCTCTCACTATCACTTCCCATCTTTGTTAGTTGAATATATATATATATATATATATAT 110
Db 1 GGCTCTCACTATCACTTCCCATCTTTGTTAGTTGAATATATATATATATATATATATAT 60
QY 111 GATCATGCTTTTCTCTTACAGAGGAGAAATTTCAATTTTACCTGAGCAAAATGATTA 170
Db 61 GATCATGCTTTTCTCTTACAGAGGAGAAATTTCAATTTTACCTGAGCAAAATGATTA 120
QY 171 GAAATGAACCACTAGAGATATATATGTTTGAAGAAATTAAGTATTTCTTAAAGGCC 230
Db 121 GAAATGAACCACTAGAGATATATATGTTTGAAGAAATTAAGTATTTCTTAAAGGCC 180
QY 231 CAGCCCTGACAAATTTGTAAGTAAATCTCACTGTCTCATGATGATATGTTG 290
Db 181 CAGCCCTGACAAATTTGTAAGTAAATCTCACTGTCTCATGATGATATGTTG 240
QY 291 TCCACTATGCACTATCACTCAATTTTCCCTCTTACAGACATTCATCTTCCGAT 350
Db 241 TCCACTATGCACTATCACTCAATTTTCCCTCTTACAGACATTCATCTTCCGAT 300
QY 351 CTTCTTGTCTTCCCAACCAAAACATCATGTTTATATAGTTCGTATACAGTACAGATC 410
Db 301 CTTCTTGTCTTCCCAACCAAAACATCATGTTTATATAGTTCGTATACAGTACAGATC 360
QY 411 TTTGTCTACTCTATCAAGAGCCAGTACCACTCATGAAAGAAACACAGAGTACG 470
Db 361 TTTGTCTACTCTATCAAGAGCCAGTACCACTCATGAAAGAAACACAGAGTACG 420
QY 471 TGAAGAGCTAAACATCATCAAAACACATCTCTTCTCTCACTTCTCTCACTCT 530
Db 421 TGAAGAGCTAAACATCATCAAAACACATCTCTTCTCTCACTTCTCTCACTCT 480
QY 531 TTACCTTTTCCAAATCCCAATCCCAATCAATTTTCTCTTCTTCTTCTCTCTCC 590
Db 481 TTACCTTTTCCAAATCCCAATCCCAATCAATTTTCTCTTCTTCTTCTCTCTCC 540
QY 591 TTTTACCTTCCATGCTGTTTAAAGAGAGATGGAGATCAATCTGTATATCTTCTGA 650
Db 541 TTTTACCTTCCATGCTGTTTAAAGAGAGATGGAGATCAATCTGTATATCTTCTGA 600
QY 651 CACAGTTATACATGCTATCAAAACCAAGCTTCTCATAGTGAAGATCTTCTTCTAG 710
Db 601 CACAGTTATACATGCTATCAAAACCAAGCTTCTCATAGTGAAGATCTTCTTCTAG 660
QY 711 AACATAGGATGAAGTAAAGTCTGCTGAAAGTTTGGGGGAAAGTTTCTTCTGAGAGTT 770
Db 661 AACATAGGATGAAGTAAAGTCTGCTGAAAGTTTGGGGGAAAGTTTCTTCTGAGAGTT 720
QY 771 AAGTATTTTAG 830

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Db	121	GAAAAATGAAACCACTAGAGGAATATAAGTGTGAGAAATTAAGTCAATTTCTAAGGGCC	180
QY	231	CAGCCCTTGACAAATAATGTGAAAGTTAAATTCCTCACTGTGTCCATCAGATCTAATGTTC	290
Db	181	CAGCCCTTGACAAATAATGTGAAAGTTAAATTCCTCACTGTGTCCATCAGATCTAATGTTC	240
QY	291	TTCCATATGGAACCTAAGTCACTCAATTTTCCCTCTTGAGAGCAATTCATTTCCCAT	350
Db	241	TTCCATATGGAACCTAAGTCACTCAATTTTCCCTCTTGAGAGCAATTCATTTCCCAT	300
QY	351	CTTCTTTGCTCTCTCCAAACCAAAACATCAATGTTATTAAGTCTGTAATCAGTACAGATC	410
Db	301	CTTCTTTGCTCTCTCCAAACCAAAACATCAATGTTATTAAGTCTGTAATCAGTACAGATC	360
QY	411	TTTGGTCTACTCTATCAAGAGGCCAGTACCACTACATGAAAGAAACAAGAGTAGC	470
Db	361	TTTGGTCTACTCTATCAAGAGGCCAGTACCACTACATGAAAGAAACAAGAGTAGC	420
QY	471	TGAGAGGCTAAAACTCATCAAAAAACATGATCTCTTTCTCTACCTATTTCTCTCAATCTT	530
Db	421	TGAGAGGCTAAAACTCATCAAAAAACATGATCTCTTTCTCTACCTATTTCTCTCAATCTT	480
QY	531	TTACTCTTTTCAAAATCCCAATCCCAATCAATGTTTTCTCTTCTACCTCCCTCTGCC	590
Db	481	TTACTCTTTTCAAAATCCCAATCCCAATCAATGTTTTCTCTTCTACCTCCCTCTGCC	540
QY	591	TTTTACCCCTCATGTGTGTTAAAGAGAGATGGGAGAGCATTTCTGTATTAATCTTGTA	650
Db	541	TTTTACCCCTCATGTGTGTTAAAGAGAGATGGGAGAGCATTTCTGTATTAATCTTGTA	600
QY	651	CACAGTTATACATGTCTATCAAAACCCAGACTTGCTTCATATGAGAGCTTGCTTTCAAG	710
Db	601	CACAGTTATACATGTCTATCAAAACCCAGACTTGCTTCATATGAGAGCTTGCTTTCAAG	660
QY	711	AACATATGGAATGAATAGATGCCGGAAGATTTGGGGGAAAAGTTTCTTCAGAGAGTT	770

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Ddb	1021 CTAGTAGACCTTTGAGGAGATTCAACAGTGTCTTCAGCAGGTTCAGAGCCAGC	1086
Oy	1131 AAGAGTTGAAGTTGCTTAGACCAAGGACATAAGTATCATGTCTCCTTTAACTAGCAT	1199
Ddb	1081 AAGAGTTGAAGTTGCTTAGACCAAGGACATAAGTATCATGTCTCCTTTAACTAGCAT	1149
Oy	1191 CCCCAAGTGGAGAGAGGGTGCAGCGCTCAAGGCATTAAGTCATTCCAAATCAGCAACT	1256
Ddb	1141 CCCCAAGTGGAGAGAGGGTGCAGCGCTCAAGGCATTAAGTCATTCCAAATCAGCAACT	1200

Db 1201 AAGTGTCTTTTCGTTGCTGTCACCATGGAACATTTGATTATAGTAACTCTTC 1260
Qy 1311 TATCTGAATCTT 1323
Db 1261 TATCTGAATCTT 1273

RESULT 13
US-09-328-925-79
; Sequence 79, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-79

Query Match 74.2%; Score 1266.6; DB 3; Length 1273;
Best Local Similarity 99.7%; Pred. No. 6.5e-307;
Matches 1269; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 51 GAGCCTCACTAATATCACTTCCCATCTTTGTTGATTTGAATATATACATTTCTAT 110
Db 1 GAGCCTCACTAATATCACTTCCCATCTTTGTTGATTTGAATATATACATTTCTAT 60

Qy 111 GATCATTTGCTTTCTTTTACAGGGAGAAATTTGATTTTACCTGAGCAATTTGATTA 170
Db 61 GATCATTTGCTTTCTTTTACAGGGAGAAATTTGATTTTACCTGAGCAATTTGATTA 120

Qy 171 GAAATGGAACCACTAGAGAAATATATGTTGATGAAATTAACATTTCTAAGGCC 230
Db 121 GAAATGGAACCACTAGAGAAATATATGTTGATGAAATTAACATTTCTAAGGCC 180

Qy 231 CAGCCCTTGACAAATTTGTAAGTTAATTTCTCACTCTGTCATCAGATCTAATGTTTC 290
Db 181 CAGCCCTTGACAAATTTGTAAGTTAATTTCTCACTCTGTCATCAGATCTAATGTTTC 240

Qy 291 TCCACTATGGAACATACTCACTCAATTTTCCCTCTTAGAGAGATTCATCTTCCGAT 350
Db 241 TCCACTATGGAACATACTCACTCAATTTTCCCTCTTAGAGAGATTCATCTTCCGAT 300

Qy 351 CTTCTTGTCTTCTCAACCAAAATCAATGTTTATATGTTCTGTATACATACAGATC 410
Db 301 CTTCTTGTCTTCTCAACCAAAATCAATGTTTATATGTTCTGTATACATACAGATC 360

Qy 411 TTTGGTCACTCTATCAAGAGCCAGTACACATCATGAGAGAAACACAGAGATGAC 470
Db 361 TTTGGTCACTCTATCAAGAGCCAGTACACATCATGAGAGAAACACAGAGATGAC 420

Qy 471 TGAAGAGCTAAACTCATCAAAAAACATACTCTTTTCTCTACCTATTCCTCAATCTT 530
Db 421 TGAAGAGCTAAACTCATCAAAAAACATACTCTTTTCTCTACCTATTCCTCAATCTT 480

Qy 531 TTACCTTTTCAAAATCCCAATCCCAATGATTTTCTCTTCTAATCCCTCTCC 590
Db 481 TTACCTTTTCAAAATCCCAATCCCAATGATTTTCTCTTCTAATCCCTCTCC 540

Qy 591 TTTTACCTTCATGCTGTTAAAGAGATGAGGAGATCATTTCTGTTATCTTCTGTA 650
Db 541 TTTTACCTTCATGCTGTTAAAGAGATGAGGAGATCATTTCTGTTATCTTCTGTA 600

Qy 651 CACAGTTATACATGCTATCAAAACCCAGACTTGCTTCCATAGTGAAGACTTCTTCAG 710
Db 601 CACAGTTATACATGCTATCAAAACCCAGACTTGCTTCCATAGTGAAGACTTCTTCAG 660

Qy 711 AACATAGGATGAAAGTAAAGTGTCTGAAAAGTTTGGGGAAAAGTTTCTTTCAGAGATT 770
Db 661 AACATAGGATGAAAGTAAAGTGTCTGAAAAGTTTGGGGAAAAGTTTCTTTCAGAGATT 720

Qy 771 AAGTATTTTAG 830
Db 721 AAGTATTTTAG 780

Qy 831 TGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 890
Db 781 TGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

Qy 891 AGCCATTTTAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 950
Db 841 AGCCATTTTAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900

Qy 951 AGATTGGCATATCATTTGTAATAAAGCTGACATTTGACCCAGATATATGTAATCTTCTT 1010
Db 901 AGATTGGCATATCATTTGTAATAAAGCTGACATTTGACCCAGATATATGTAATCTTCTT 960

Qy 1011 CTAAATAATAG 1070
Db 961 CTAAATAATAG 1020

Qy 1071 CTATAGAGACTTTGAGAGAAATTTCAACAGTGTCTTTCAGAGTTCAGAGCCAAAGC 1130
Db 1021 CTATAGAGACTTTGAGAGAAATTTCAACAGTGTCTTTCAGAGTTCAGAGCCAAAGC 1080

Qy 1131 AAGAAGTTGAAGTGTCTAGACAGAGACATATGATCATGTCTCTTCTTAACTAGACATA 1190
Db 1081 AAGAAGTTGAAGTGTCTAGACAGAGACATATGATCATGTCTCTTCTTAACTAGACATA 1140

Qy 1191 CCCGAAAGTGAAGAGGGGTGACAGAGCTCAAAAGGCAATTTCCATCAGCCAACT 1250
Db 1141 CCCGAAAGTGAAGAGGGGTGACAGAGCTCAAAAGGCAATTTCCATCAGCCAACT 1200

Qy 1251 AAGTGTCTTCTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG 1310
Db 1201 AAGTGTCTTCTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG 1260

Qy 1311 TATCTGAATCTT 1323
Db 1261 TATCTGAATCTT 1273

RESULT 14
US-09-328-925-82
; Sequence 82, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-82

Query Match 73.9%; Score 1261; DB 3; Length 1272;

Best Local Similarity: 99.9%; Pred. No. 1.6e-305;
Matches 1272; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 51 GGCCTCTCACTAATCACTTCCCATCTTTGTGATTTGAATATATACATTCAT 110
DB 1 GGCCTCTCACTAATCACTTCCCATCTTTGTGATTTGAATATATACATTCAT 60
OY 111 GATCATTCCTTTCTTTTCAAGGGGAATTCATATTTTAACTGAGCAATGATTA 170
DB 61 GATCATTCCTTTCTTTTCAAGGGGAATTCATATTTTAACTGAGCAATGATTA 120
OY 171 GAAATGGAACCACTAGAGAAATATATGTGTAGAAATTAACATCAATTCAGGCC 230
DB 121 GAAATGGAACCACTAGAGAAATATATGTGTAGAAATTAACATCAATTCAGGCC 180
OY 231 CAGCCCTTGACAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAATATGTTTC 290
DB 181 CAGCCCTTGACAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAATATGTTTC 240
OY 291 TCCACTATGGCACTAATCACTCAATTTCCCTGCTAGAGCAATTCATCTCCGAT 350
DB 241 TCCACTATGGCACTAATCACTCAATTTCCCTGCTAGAGCAATTCATCTCCGAT 300
OY 351 CTCTCTTCTCTCCACCAAAACATCAATGTTTATAGTTCTGTATACAGTACAGATC 410
DB 301 CTCTCTTCTCTCCACCAAAACATCAATGTTTATAGTTCTGTATACAGTACAGATC 360
OY 411 TTTGTCTACTCTATCAAGGCCAGTACACACTCTATGAGAGAAACACAGAGTACC 470
DB 361 TTTGTCTACTCTATCAAGGCCAGTACACACTCTATGAGAGAAACACAGAGTACC 420
OY 471 TGAAGGCTAAACATCAAAACATCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 530
DB 421 TGAAGGCTAAACATCAAAACATCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
OY 531 TTACCTTTTCCAAATCCCAATCCCAATCACTTTTCTCTTCTTCTCTCTCTCTCC 590
DB 481 TTACCTTTTCCAAATCCCAATCCCAATCACTTTTCTCTTCTTCTCTCTCTCTCC 540
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DB 541 TTTTACCTTCATGCTCTTAAAGAGAGATGGAGATCACTCTGTTATATCTCTGTA 600
OY 651 CACAGTTTATACATGCTATCAAAACCACTGCTTCCATGATGAGACCTGCTTTGAG 710
DB 601 CACAGTTTATACATGCTATCAAAACCACTGCTTCCATGATGAGACCTGCTTTGAG 660
OY 711 AACATAGGAGATGAAAGTATGCTGAAAGGTTGGGGGAAAAGTTCTTTCAAGAGTT 770
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OY 891 AGCCATTTCAAGAGCTTGTATGTTATGAGAGTCTGACTAGGACATGATTTCCAGAGCA 950
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OY 951 AGATTGGCATATCATTTGTAATTAAGCTGACATTCAGCCAGACATATGTATCTCTTT 1010
DB 901 AGATTGGCATATCATTTGTAATTAAGCTGACATTCAGCCAGACATATGTATCTCTTT 960
OY 1011 CTAATAAATAATATATATATATATATATATATATATATATATATATATATATAT 1070
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DB 1081 AAGAAGTTAAGTTCCTTAGACCAAGAGACATTAATATCATGTCTCTTAACTAGCATTA 1140
OY 1191 CCCGAGTGTGAGAGAGGTGTGAGAGGCTCAAGAGCATTAAGTCAATTCAGAGCAACT 1250
DB 1141 CCCGAGTGTGAGAGAGGTGTGAGAGGCTCAAGAGCATTAAGTCAATTCAGAGCAACT 1200
OY 1251 AAGTTGTCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1310
DB 1201 AAGTTGTCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1259
OY 1311 TATCTGAAATCTT 1323
DB 1260 TATCTGAAATCTT 1272
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RESULT 15

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US-09-328-925-80
; Sequence 80, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: US-03603
; CURRENT APPLICATION NUMBER: US/09/328, 925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-80
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Query Match 73.9%; Score 1261; DB 3; Length 1275;
Best Local Similarity 99.8%; Pred. No. 1.6e-305;
Matches 1273; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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DB 1 GGCCTCTCACTAATCACTTCCCATCTTTGTGATTTGAATATATACATTCAT 60
OY 111 GATCATTCCTTTCTTTTCAAGGGGAATTCATATTTTAACTGAGCAATGATTA 170
DB 61 GATCATTCCTTTCTTTTCAAGGGGAATTCATATTTTAACTGAGCAATGATTA 120
OY 171 GAAATGGAACCACTAGAGAAATATATGTGTAGAAATTAACATCAATTCAGAGGCC 230
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OY 350 -TCTTCTTCTCTCTCCACCAAAACATCAATGTTTATATGTTCTGTATACAGTACAGGA 408
DB 301 TCTTCTTCTCTCTCTCCACCAAAACATCAATGTTTATATGTTCTGTATACAGTACAGGA 360
OY 409 TCTTGTGTCTCTCTATCAAGGCCAGTACCACTCATGATGAGAAAGACAGAGATA 468
DB 361 TCTTGTGTCTCTCTATCAAGGCCAGTACCACTCATGATGAGAAAGACAGAGATA 420
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DB 421 GCTGAGAGCTTAAATCATCAAAAACATCTCTTTCTCTACCTTATCTCAATC 480
QY 529 TTTTACCTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATC 588
DB 481 TTTTACCTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATC 540
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DB 541 CCTTTTACCTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATC 600
QY 649 TACACAGTTATACATGCTATCAAAACCAAGCTTCTTCAATGAGACTTCTTTC 708
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QY 709 AGAACATAGGATGAG 768
DB 661 AGAACATAGGATGAG 720
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DB 721 TTAAGTTATTTAT 780
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DB 841 TAAAGCATTTTAAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTT 900
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DB 961 TTTCTAAAAAT 1020
QY 1069 AGCTAGTAGAGACTTTGAGAGAAATTCACAGTGTGCTTCAAGAGGTTCAGAGCCAA 1128
DB 1021 AGCTAGTAGAGACTTTGAGAGAAATTCACAGTGTGCTTCAAGAGGTTCAGAGCCAA 1080
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DB 1081 GCAAGAAAGTTGAGCTTGTAGACCAAGGACATTAATGATCATGCTTTTAACTAGCA 1140
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DB 1141 TACCCCGAAGTGAAG 1200
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QY 1309 TCTATCTTGAATCTT 1323
DB 1261 TCTATCTTGAATCTT 1275

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Job time : 365.148 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 12:46:08 ; Search time 1699.66 Seconds
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Title: US-09-884-901A-7

Perfect score: 1707
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Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	1707	US-09-884-901-7	Sequence 7, Appli
2	1701.8	99.7	38059	US-09-880-107-2125	Sequence 2125, Ap
3	1687	98.8	44752	US-10-741-600-17553	Sequence 17553, A
4	1391	81.5	1400	US-10-956-157-5592	Sequence 5592, Ap
5	1391	81.5	1400	US-11-060-756-1937	Sequence 1937, Ap
6	1391	81.5	1400	US-11-060-756-6209	Sequence 6209, Ap
7	1391	81.5	2804	US-10-133-829-2	Sequence 2, Appli
8	1391	81.5	2804	US-10-133-907-2	Sequence 357, App
9	1391	81.5	2804	US-10-956-157-357	Sequence 357, App
10	1391	81.5	2804	US-10-804-763-40	Sequence 40, Appli
11	1387.8	81.3	2792	US-09-118-748-1	Sequence 16, Appli
12	1377	80.7	2728	US-10-349-858-16	Sequence 3, Appli
13	1376.6	80.6	2728	US-10-741-600-3	Sequence 1, Appli
14	1376.6	80.6	2728	US-10-741-600-1	Sequence 2, Appli
15	1376.6	80.6	2728	US-10-741-600-2	Sequence 2, Appli
16	1376.6	80.6	2831	US-10-741-600-4	Sequence 4, Appli
17	933.4	54.7	1971	US-09-864-761-13921	Sequence 13921, A
18	236	13.8	1438	US-10-038-854-5	Sequence 5, Appli
19	229.8	13.5	581	US-09-925-065A-808251	Sequence 808251, A
20	200.6	11.8	201	US-10-741-600-1929	Sequence 1929, Ap
21	200.6	11.8	201	US-10-741-600-2210	Sequence 2210, Ap
22	200.6	11.8	201	US-10-741-600-2492	Sequence 2492, Ap
23	200.6	11.8	201	US-10-741-600-2779	Sequence 2779, Ap

24	200.6	11.8	201	US-10-741-600-18209	Sequence 18209, A
25	200.6	11.8	201	US-10-741-600-18362	Sequence 18362, A
26	172.4	10.1	422	US-09-960-352-12761	Sequence 12761, A
27	160	9.4	1610	US-10-073-064-6	Sequence 6, Appli
28	160	9.4	13928	US-10-362-916-1	Sequence 1, Appli
29	159	9.3	1548	US-09-150-811-6	Sequence 6, Appli
30	94.2	5.5	370	US-09-960-352-11540	Sequence 11540, A
31	89	5.2	201	US-10-741-600-1867	Sequence 1867, Ap
32	89	5.2	201	US-10-741-600-2148	Sequence 2148, Ap
33	89	5.2	201	US-10-741-600-2431	Sequence 2431, Ap
34	89	5.2	201	US-10-741-600-2717	Sequence 2717, Ap
35	89	5.2	201	US-10-741-600-18262	Sequence 18262, A
36	86.4	5.1	555	US-09-925-065A-308075	Sequence 308075, A
37	86.4	5.1	1758	US-09-925-065A-58792	Sequence 58792, A
38	86	5.0	528	US-09-925-065A-100582	Sequence 100582, A
39	85.4	5.0	473	US-09-814-353-18136	Sequence 18136, A
40	85	5.0	201	US-10-741-600-1847	Sequence 1847, Ap
41	85	5.0	201	US-10-741-600-2128	Sequence 2128, Ap
42	85	5.0	201	US-10-741-600-2411	Sequence 2411, Ap
43	85	5.0	201	US-10-741-600-2697	Sequence 2697, Ap
44	85	5.0	201	US-10-741-600-18236	Sequence 18236, A
45	84	4.9	2502	US-10-676-248B-37	Sequence 37, Appli

ALIGNMENTS

RESULT 1					
US-09-884-901-7					
Sequence 7, Application US/09884901					
Patent No. US20020076798A1					
GENERAL INFORMATION:					
APPLICANT: Miao, Carol					
APPLICANT: Kay, Mark					
TITLE OR INTENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use					
FILE REFERENCE: US-09-884,901					
CURRENT FILING DATE: 2001-06-18					
PRIOR APPLICATION NUMBER: US 60/212,902					
PRIOR FILING DATE: 2000-06-20					
NUMBER OF SEQ ID NOS: 18					
SOFTWARE: PatentIn version 3.0					
SEQ ID NO 7					
LENGTH: 1707					
TYPE: DNA					
ORGANISM: Homosapien					
US-09-884-901-7					
Query Match					
Best Local Similarity 100.0%; Score 1707; DB 3; Length 1707;					
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	AATGAAGATGATTCAGAGTTTCAAGTTTCAATTCATTCGTAATGAAATTAAGAGGCTCTCAC	60		
DB	1	AATGAAGATGATTCAGAGTTTCAAGTTTCAATTCATTCGTAATGAAATTAAGAGGCTCTCAC	60		
QY	61	TAACTAATCACTTCCATCTTTTGTGATTTGAATTAATTAATTCATTCATTCATTCGTT	120		
DB	61	TAACTAATCACTTCCATCTTTTGTGATTTGAATTAATTAATTCATTCATTCATTCGTT	120		
QY	121	TTTCTCTTTCACAGGAGAAATTTCAATTTTAACTAGGAGAAATTTAGAAATTTAGAA	180		
DB	121	TTTCTCTTTCACAGGAGAAATTTCAATTTTAACTAGGAGAAATTTAGAAATTTAGAA	180		
QY	181	CCACTAGAGGATTAATTAATTTAGAAATTAATTCATTCATTCATTCATTCATTCATTC	240		
DB	181	CCACTAGAGGATTAATTAATTTAGAAATTAATTCATTCATTCATTCATTCATTCATTC	240		
QY	241	CAAAATTTGAGATTAATTTCACTCTGTCATCAATTAATTAATTTAGGCTTTTCTT	300		
DB	241	CAAAATTTGAGATTAATTTCACTCTGTCATCAATTAATTAATTTAGGCTTTTCTT	300		
QY	301	CAACTAATCACTCAATTTTCCCTCTTGAAGAGATTCATTCCTCCATCTTTTCTT	360		
DB	301	CAACTAATCACTCAATTTTCCCTCTTGAAGAGATTCATTCCTCCATCTTTTCTT	360		

[illegible]

Db	1381	TTCTGCGTTCATACCTTGGCTTTTGTGGATTCATATGATGAAATCAGATCAACCCGTATT	1440
Qy	1441	TGATATATGCAATGGAGACTCTATGACAAATATCATCTTGAACCCCTGGCAAGCTGCTGCTTCTCC	1500
Db	1441	TGATATATCATAAGGAGACTATCTGACAAATATCATCTTGAACCCCTGGCAAGCTGCTGCTTCTCC	1500
Qy	1501	TGCCCAACTCATACCCGAGCGAGGCGCTCATCTGTGATGTTCCCTTAAGTCTTTTAGTC	1560
Db	1501	TGCCCAACTCATACCCCGAGCGAGGCGCTCATCTGTGATGTTCCCTTAAGTCTTTTAGTC	1560
Qy	1561	AATATATTTTGTCTTGCGCATATATAGATATATATTAATATTTTAAATTTCTTGGCTGG	1620
Db	1561	AATATATTTTGTCTTGCGCATATATAGATATATTAATATTAATTTTAAATTTCTTGGCTGG	1620
Qy	1621	GCCCAAGTGGCTCAGCGCTATATATCCAGCACTTCTGAGAGGCCAGAGTGAGGCGATCACT	1680
Db	1621	GCCCAAGTGGCTCAGCGCTATATATCCAGCACTTCTGAGAGGCCAGAGTGAGGCGATCACT	1680
Qy	1681	GAGGTAGAGATTTCAAGGCCAAAGTTA	1707
Db	1681	GAGGTAGAGATTTCAAGGCCAAAGTTA	1707

	RESULT 2	
US-09-880-107-2125		
/ Sequence 2125, Application US/09880107		
/ Patent No. US20020142981A1		
/ GENERAL INFORMATION:		
/ APPLICANT: Horne, Darci T.		
/ APPLICANT: Vockley, Joseph G.		
/ APPLICANT: Scherf, Uwe		
/ APPLICANT: Gene Logic, Inc.		
/ TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer		
/ FILE REFERENCE: 44921-5028-MO		
/ CURRENT APPLICATION NUMBER: US/09/880,107		
/ PRIOR FILING DATE: 2001-06-14		
/ PRIOR APPLICATION NUMBER: US 60/211,379		
/ PRIOR FILING DATE: 2000-06-14		
/ PRIOR APPLICATION NUMBER: US 60/227,054		
/ NUMBER OF SEQ ID NOS: 3950		
/ SOFTWARE: PatentIn Ver. 2.1		
/ SEQ ID NO 2125		
/ LENGTH: 38059		
/ TYPE: DNA		
/ ORGANISM: Homo sapiens		
/ FEATURE:		
/ OTHER INFORMATION: Genbank Accession No. US20020142981A1 K02402		
US-09-880-107-2125		
Query Match	99.7%; Score 1701.8; DB 3; Length 38059;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 1703; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 AATGAAAGATGATTTCCAGGTAAATTCATTGGAATTGAAAATTACAGGGCCTCTCAC	60
Dd	34333 AATGAAAGATGATTTCCAGGTAAATTCATTGGAATTGAAAATTACAGGGCCTCTCAC	34339
Qy	61 TAACTAATCACTTCCCATTCTTTTGTTAGAATTGGAATAATATATACATCTCATGATCTTGC	120
Dd	34393 TAACTAATCACTTCCCATTCTTTTGTTAGAATTGGAATAATATATACATCTCATGATCTGC	34455
Qy	121 TTTCCTTTACAGGGGAGAAATTCATATTTTAPCTGAGCAAATTGATTAGAAAAATGAA	180
Dd	34453 TTTCCTTTACAGGGGAGAAATTCATATTTTACTGAGCAAATTGATTAGAAAAATGAA	34512
Qy	181 CCACTAGAGGAATTAATGTGTGTAGAAAATTACAGTCAATTTCTTAAGGCCCGACCCTTGA	240
Dd	34513 CCACTAGAGGAATTAATGTGTGTAGAAAATTACAGTCAATTTCTTAAGGCCCGACCCTTGA	34572
Qy	241 CAATAATTTGAAATTAATTTCTTCCAATCTGTGCATATAGATATACATAGTCTTCCATATGG	300
Dd	34573 CAATAATTTGAAATTAATTTCTTCCAATCTGTGCATATAGATATACATAGTCTTCCATATGG	34632

[illegible]

Oy	1381	CTCGGTCATACCTTGCGCTTTTGTGAGATCCATGTAGTAATCAAGTCAACCTGTAT	1440
Db	35713	TTCTGGTTCATACCTTGCGCTTTTGTGAGATCCATGTAGTAATCAAGTCAACCTGTAT	35777
Oy	1441	TGATGATGCATGGGACTACTGACAAATTCATCTGACCCCTGCGCAAGCTGCTGCTTCC	15000
Db	35773	TGATGATGCATGGGACTACTGACAAATTCATCTGACCCCTGCGCAAGCTGCTGCTTCC	35833
Oy	1501	TGCCCCAAGCTCAACCCCGACGAGGCGCTCACTCTTGCTAGTTCTTTAGTTCTTTTAGTC	15666
Db	35893	TGCCCCAAGCTCAACCCCGACGAGGCGCTCACTCTTGCTAGTTCTTTAGTTCTTTTAGTC	35899
Oy	1561	AATATATTTTTGTCTTGCGCATATTAAGTTAAATTAATTTTAAATTTCTTGCGCGG	16280
Db	35893	AATATATTTTTGTCTTGCGCATATTAAGTTAAATTAATTTTAAATTTCTTGCGCGG	35899
Oy	1621	GCCCAAGTGGCTCAAGCCTATTAATCCAGCACTTCTGAGGCGCAGATGGCGGATCACT	16800
Db	35953	GCCCAAGTGGCTCAAGCCTATTAATCCAGCACTTCTGAGGCGCAGATGGCGGATCACT	36010
Oy	1681	GAGGTAGAGATTTCAAGGCCAAGCT	1705
Db	36013	GAGGTAGAGATTTCAAGGCCAAGCT	36037

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RESULT 3
US-10-741-600-17553
; Sequence 17553, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17553
; LENGTH: 44752
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(44752)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
; US-10-741-600-17553

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	Query Match	98.8% ; Score 1687; DB 8; Length 44752;
	Best Local Similarity 99.6% ; Pred. No. 0;	
	Matches 1699; Conservative 2; Mismatches 2; Indels 2; Gaps 1;	
QY	1 AATGAAGATGCGATTTCCAGGTGTAATTCATATGGAATTGAAATTAACAGGGCCTCTCAC	60
Db	37365 AATGAAAGATGCGATTTCCAGGTGTAATTCATATGGAATTGAAATTAACAGGGCCTCTCAC	37422
QY	61 TAACTAATCACTTTCCTTCATCTTTTGTGATGATTGAAATATATACCTTATGATCATTTGCT	120
Db	37425 TAACTAATCACTTTCCTTCATCTTTTGTGATGATTGAAATATATACCTTATGATCATTTGCT	37488
QY	121 TTTTCTCTTTACAGGGGGAATTTTCATATTTTACCTGAGCAAAATGATTTGAAANAATGAA	180
Db	37485 TTTTCTCTTTACAGGGGGAATTTTCATATTTTACCTGAGCAAAATGATTTGAAANAATGAA	3754
QY	181 CCACCTAGAGGAATTAATNGTGTAGAAATTACAGTCATTTCTAAGGGCCACGCCCTTGA	240
Db	37545 CCACCTAGAGGAATTAATNGTGTAGAAATTACAGTCATTTCTAAGGGCCACGCCCTTGA	3760
QY	241 CAAATTTGTGAAGTTAAATTTCTCCACTCTGTGCATCAGATCTAATGTTCTCCACTAATGG	300
Db	37605 CAAATTTGTGAAGTTAAATTTCTCCACTCTGTGCATCAGATCTAATGTTCTCCACTAATGG	3766
QY	301 CAACCTAACCTCAATTTTCCCTCTTACAGACATTCACATCTCCGATCTTCTTTGCT	360

[illegible]

Db	38743	TTCTGGTTCATACCTTCGCTCTTTTGTGGATTTCATATGATGTGATCAAGTCACCCCTGTATT	38802
Qy	1441	TGATGATGCGAATGGGCACTACTGACAAATCACTCGACGCGCAAGCTGTGCTCTCTCC	1500
Db	38803	TGATGATGCGATGGGACACTACTGACAAATCACTCGACGCCCAAGCTGTGCTCTCTCC	38862
Qy	1501	TGCCCCAAGCTCAACCCCGACGCGCTCACTCTGTGATGTTCTTTAAGTCTTTTAATGTC	1560
Db	38863	TGCCCCAAGCTCAACCCCGACGCGCTCACTCTGTGATGTTCTTTAAGTCTTTTAATGTC	38922
Qy	1561	AATATATTTTGTCTTGCAATTAAGATATAATTAACATATTTTAAATTTCTTGCGCTGG	1620
Db	38923	AATATATTTTGTCTTGCAATTAAGATATAATTAACATATTTTAAATTTCTTGCGCTGG	38982
Qy	1621	GCCCAAGTGGCTCAAGCCTATATATCCCAACACTTCTGAGGCCAAGTGGGGCGAATCACTT	1680
Db	38983	GCCCAAGTGGCTCAAGCCTATATATCCCAACAACAATTTTAAATTTCTTGAGGCGAATCACTT	39042
Qy	1681	GAGGTAGAGATTTCAGGCCCAAGCT	1705
Db	39043	GAGGTAGAGATTTCAGGCCCAAGCT	39067

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RESULT 4
US-10-956-157-5592
; Sequence 5592, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5592
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5592

Query Match      81.5%; Score 1391; DB 9; Length 1400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AATGAAGATGAGATTTCACAGCTTAATTCATTGGAATTGAAAATTAAACAGGGCCTCTCAC 60
DB      10  AATAAAGATGAGATTTCACAGGTTAATTCATTGGAATTGAAAATTAAACAGGGCCTCTCAC 69

QY      61  TAACTATCACTTCCCATCTTTGGTAGATTTGAATATATATACATCTATGATCATTTGCT 120
DB      70  TAACTATCACTTCCCATCTTTGGTAGATTTGAATATATATACATCTATGATCATTTGCT 129

QY      121  TTTTCTCTTACAGGGGAGAATTCATATTTTAACTGAGCAAAATTGATGAAAATGAAA 180
DB      130  TTTTCTCTTACAGGGGAGAATTCATATTTTAACTGAGCAAAATTGATGAAAATGAAA 189

QY      181  CCACTAGAGAAATATATGTGTAGAGAAATTAAAGCATTTCTAAAGGCCACAGCCCTGA 240
DB      190  CCACTAGAGAAATATATGTGTAGAGAAATTAAAGCATTTCTAAAGGCCACAGCCCTGA 249

QY      241  CAAATTTGTGAAGTTAAATCTCCACTCTGTCCATCAGATACATAGTGTCTCCACTATGG 300
DB      250  CAAATTTGTGAAGTTAAATCTCCACTCTGTCCATCAGATACATAGTGTCTCCACTATGG 309

QY      301  CAACTACTACTCATCAATTTTCCCTCTGTAGACAGATTCACATCTTCCGATCTTTGCT 360
DB      310  CAACTACTACTCATCAATTTTCCCTCTGTAGACAGATTCACATCTTCCGATCTTTGCT 369

QY      361  TCTCCACCAAAACATCAATGTTATAGTTCGTATACAGTACAGATCTTGTGCTAC 420

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Db 370 TCTCAACCAAAACATCATAGTTTATTTAGTCTGTATATACAGTACAGGATCTTTGCTAC 429
Qy 421 TCTATCAAGGCGAGTACCACTCATGTAAAGAAACAAGAGTAGTGAAGGCTA 480
Db 430 TCTATCAAGGCGAGTACCACTCATGTAAAGAAACAAGAGTAGTGAAGGCTA 489
Qy 481 AACTCATCAAAAACATCACTCTCTCTCTCACTATCTCAATCTTTTACCTTTTC 540
Db 490 AACTCATCAAAAACATCACTCTCTCTCTCACTATCTCAATCTTTTACCTTTTC 549
Qy 541 CAATCCCAATCCCAATCAATGTTTTCTCTTTCTTACTCTCTCTCTCTCTTACCTTC 600
Db 550 CAATCCCAATCCCAATCAATGTTTTCTCTTTCTTACTCTCTCTCTCTCTTACCTTC 609
Qy 601 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 660
Db 610 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 669
Qy 661 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 720
Db 670 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 729
Qy 721 TGAAGTAGGCTGCTGAAAGATTGGGGGAAAGTTCTTTCAAGAGTTAAGTTATTT 780
Db 730 TGAAGTAGGCTGCTGAAAGATTGGGGGAAAGTTCTTTCAAGAGTTAAGTTATTT 789
Qy 781 AT 840
Db 790 AT 849
Qy 841 TATGCTGTGTATGAGACACACACCATATACACATATATATATATATATATATATAT 900
Db 850 TATGCTGTGTATGAGACACACACCATATACACATATATATATATATATATATATAT 909
Qy 901 AGAGCTGTATGTATATGAGAGTCTGACTAGGCAATGATTTCAAGAGCAAGATTGCA 960
Db 910 AGAGCTGTATGTATATGAGAGTCTGACTAGGCAATGATTTCAAGAGCAAGATTGCA 969
Qy 961 ATCATGTGTAT 1020
Db 970 ATCATGTGTAT 1029
Qy 1021 TAT 1080
Db 1030 TAT 1089
Qy 1081 CTTTGAGAGAAATTCACAGATGTGTCTTCAAGAGTGTTCAGAGCAAGAAAGTTGA 1140
Db 1090 CTTTGAGAGAAATTCACAGATGTGTCTTCAAGAGTGTTCAGAGCAAGAAAGTTGA 1149
Qy 1141 AGTTGCGTATGACAGAGAGCATATAGTATCATGTCTCTTAACTAGCATACCCGAAAGTG 1200
Db 1150 AGTTGCGTATGACAGAGAGCATATAGTATCATGTCTCTTAACTAGCATACCCGAAAGTG 1209
Qy 1201 GAGAGAGGTGACAGAGGCTCAAGAGCATATAGTATCATATCAAGCACTAAGTTGCTCT 1260
Db 1210 GAGAGAGGTGACAGAGGCTCAAGAGCATATAGTATCATATCAAGCACTAAGTTGCTCT 1269
Qy 1261 TTTCTGTTTGTGTTCACATGAACTTTTGAATATATATATATATATATATATATATAT 1320
Db 1270 TTTCTGTTTGTGTTCACATGAACTTTTGAATATATATATATATATATATATATATAT 1329
Qy 1321 CTTCAGAGAGGTGCTGACAACTGAGATGATTTCCCTTTGTGAATTAATAACTGCTG 1380
Db 1330 CTTCAGAGAGGTGCTGACAACTGAGATGATTTCCCTTTGTGAATTAATAACTGCTG 1389
Qy 1381 TTTCTGTTTGTAT 1391
Db 1390 TTTCTGTTTGTAT 1400

RESULT 5
US-11-060-756-1937

; Sequence 1937, Application US/11060756
; Publication No. US2005021354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ. ID NOS: 303284
; SOFTWARE: Patentin version 3.2
; SEQ. ID NO 1937
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-1937

Query Match 81.5%; Score 1391; DB 10; Length 1400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATGAAAGATGATTTCCAAAGTTAATTCATGGAATTTGAAATTAACAGGGCTCTAC 60
Db 10 AATGAAAGATGATTTCCAAAGTTAATTCATGGAATTTGAAATTAACAGGGCTCTAC 69
Qy 61 TAACTATCACTTTCCATCTTTTGTATATGAAATATATATATATATATATATATATAT 120
Db 70 TAACTATCACTTTCCATCTTTTGTATATGAAATATATATATATATATATATATATAT 129
Qy 121 TTTTCTCTTACAGGGGAAATTCATATTTTACCTGAGCAATTTGAAATGAAATGAA 180
Db 130 TTTTCTCTTACAGGGGAAATTCATATTTTACCTGAGCAATTTGAAATGAAATGAA 189
Qy 181 CCACTAGAGAAATATATATGTTAGAAATTAACAGTATTTCTAAGGGCCCAAGCTTTGA 240
Db 190 CCACTAGAGAAATATATATGTTAGAAATTAACAGTATTTCTAAGGGCCCAAGCTTTGA 249
Qy 241 CAATATGTGAAAGTTAATTTCTCACTCTGTCCATCATATATATATATATATATATAT 300
Db 250 CAATATGTGAAAGTTAATTTCTCACTCTGTCCATCATATATATATATATATATATAT 309
Qy 301 CAATATCTCATATTTTCCCTCTTACAGAGATCCATCTCCGATCTTTGCT 360
Db 310 CAATATCTCATATTTTCCCTCTTACAGAGATCCATCTCCGATCTTTGCT 369
Qy 361 TCTCCAAACCAAAACATCAATGTTATATAGTTCTGTATATACAGATCTTTGCTAC 420
Db 370 TCTCCAAACCAAAACATCAATGTTATATAGTTCTGTATATACAGATCTTTGCTAC 429
Qy 421 TCTATCAAGGCGAGTACCACTCATGTAAGAAAGAAACAAGAGTAGTGAAGGCTA 480
Db 430 TCTATCAAGGCGAGTACCACTCATGTAAGAAAGAAACAAGAGTAGTGAAGGCTA 489
Qy 481 AACTCATCAAAAACATCACTCTCTCTCTCACTATCTCAATCTTTTACCTTTTC 540
Db 490 AACTCATCAAAAACATCACTCTCTCTCTCACTATCTCAATCTTTTACCTTTTC 549
Qy 541 CAATCCCAATCCCAATCAATGTTTTCTCTTTCTTACTCTCTCTCTCTCTTACCTTC 600
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Qy 601 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 660
Db 610 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 669
Qy 661 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 720
Db 670 CATGCTGTAAAGAGAGATGGGAGAGATCATCTGTATATACCTGTATACAGATTATA 729
Qy 721 TGAAGTAGGCTGCTGAAAGATTGGGGGAAAGTTCTTTCAAGAGTTAAGTTATTT 780
Db 730 TGAAGTAGGCTGCTGAAAGATTGGGGGAAAGTTCTTTCAAGAGTTAAGTTATTT 789

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RESULT 6
US-11-060-756-6209
; Sequence 6209, Application US/11060756
; Publication No. US2005022354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6209
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-6209

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Qy	61	TAACATTAACATTTTCCCATCTTTTGTGTAGATTGAAATATATACATTATATGATCATTTGCT	120
Db	70	TAACATTAATCACTTCCCATCTTTTGTGTAAATTTGAATATATACATTTATATGATCATTTGCT	129
Qy	121	TTTTCTCTTTACAGGGGGAATTTTCATATTTTACCTGAGCAATTGATATAGAAAATGAAA	180
Db	130	TTTTCTCTTTACAGGGGGAATTTTCATATTTTACCTGAGCAATTGATATAGAAAATGAAA	189
Qy	181	CCACTAGAGAAATATATGTGTGTAGAAAATTAACGTCAATTTCTAAAGGCCACGCCCTTGA	240
Db	190	CCACTAGAGAAATATATGTGTGTAGAAAATTAACGTCAATTTCTAAAGGCCACGCCCTTGA	249
Qy	241	CAAAATTTGGAAGTTAAATCTCCACTCTGTCACATCAGATATATAGTTCTCCACTATAGG	300
Db	250	CAAAATTTGGAAGTTAAATCTCCACTCTGTCACATCAGATATATAGTTCTCCACTATAGG	309
Qy	301	CAACTAATCTCACTCAATTTTCCCTCCTTAGCAGCAATTCATCTTCCGATCTTCTTGGCT	360
Db	310	CAACTAATCTCACTCAATTTTCCCTCCTTAGCAGCAATTCATCTTCCGATCTTCTTGGCT	369
Qy	361	TCTCCAAACCAAAACATCAATGTTTATATAGTTCTGTATACAGTACAGATCTTGGTGTAC	420
Db	370	TCTCCAAACCAAAACATCAATGTTTATATAGTTCTGTATACAGTACAGATCTTGGTGTAC	429
Qy	421	TCTATACAAAGGCCAGTACCACTCACTAGAAAGAAACAAGAGTATGCTGAGAGGCTTA	480
Db	430	TCTATACAAAGGCCAGTACCACTCACTAGAAAGAAACAAGAGTATGCTGAGAGGCTTA	489
Qy	481	AAACATCATCAAAAACATCACTCTCTTCTCTCAACCTTAATCTCCATCTTTACCTTTTC	540
Db	490	AAACATCATCAAAAACATCACTCTCTTCTCTCAACCTTAATCTCCATCTTTACCTTTTC	549
Qy	541	CAAAATCCCAATCCCAAAATCAGTTTTTCTCTTCTTACTCCCTCTCTCCCTTTTACCCTTC	600
Db	550	CAAAATCCCAATCCCAAAATCAGTTTTTCTCTTCTTACTCCCTCTCTCCCTTTTACCCTTC	609
Qy	601	CATGTCGTGTAAAGAGATGAGGAGATCAATCTGTATATCTCTGTACACAGTTATTA	660
Db	610	CATGTCGTGTAAAGAGATGAGGAGATCAATCTGTATATCTCTGTACACAGTTATTA	669
Qy	661	CATGTCATCAAAACCCAGACTTGTCTTCCATATGTGAGACCTTGCTTTTCAGAACATATAGGA	720
Db	670	CATGTCATCAAAACCCAGACTTGTCTTCCATATGTGAGACCTTGCTTTTCAGAACATATAGGA	729
Qy	721	TGAAGTAAAGTGCCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATTAAGTATTTT	780
Db	730	TGAAGTAAAGTGCCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATTAAGTATTTT	789
Qy	781	AT	840
Db	790	AT	849
Qy	841	TATGCGTGTGTGTAGACACACAGCATACACATATATATAGAAAGCAATTAAGCATTTCTA	900
Db	850	TATGCGTGTGTGTAGACACACAGCATACACATATATATAGAAAGCAATTAAGCATTTCTA	909
Qy	901	AGAGCTGTATATGTGTATGTAGAGGTCTGACTAGGCAATGATTTTACAGAAAGCAAGATTGGAT	960
Db	910	AGAGCTGTATATGTGTATGTAGAGGTCTGACTAGGCAATGATTTTACAGAAAGCAAGATTGGAT	969
Qy	961	ATCATTTGTATCTAATAAAAGCTGACATTTGACCCACACATATGTACTCTTTCTAATAAATAA	1020
Db	970	ATCATTTGTATCTAATAAAAGCTGACATTTGACCCACACATATGTACTCTTTCTAATAAATAA	1029
Qy	1021	TAATATATATGTATACAGAAAAGAGAACCGTTGCTTTGCAATCTACAGCTAGTAGAGA	1080
Db	1030	TAATATATATGTATACAGAAAAGAGAACCGTTGCTTTGCAATCTACAGCTAGTAGAGA	1089
Qy	1081	CTTTGAGGAAGATTTCAACAGTGTGTCTTACAGAGTGTTCAGAGCCCAAGCAAGAAAGTTGA	1140
Db	1090	CTTTGAGGAAGATTTCAACAGTGTGTCTTACAGAGTGTTCAGAGCCCAAGCAAGAAAGTTGA	1149

QY 1141 AGTGCCTAGACACAGAGACATAAGTATCATGTCTCTTTAACTAGCATACCCGAAATG 1200
DB 1150 AGTTGCTTAGACACAGAGACATAAGTATCATGTCTCTTTAACTAGCATACCCGAAATG 1209
QY 1201 GAGAAAGGTGACAGAGGCTCAAAGGCAATAGTCAATTCAGCACTAAGTTGTCT 1260
DB 1210 GAGAAAGGTGACAGAGGCTCAAAGGCAATAGTCAATTCAGCACTAAGTTGTCT 1269
QY 1261 TTTCTGTTTCTGTTTACCAATGAAATTTGATTAATAGTTAACTCTTATCTGTAAT 1320
DB 1270 TTTCTGTTTCTGTTTACCAATGAAATTTGATTAATAGTTAACTCTTATCTGTAAT 1329
QY 1321 CTCTAGAGAGTCTGACCAACTGACGTATGTTCCCTTGTGAAATTAATTAACCTG 1380
DB 1330 CTCTAGAGAGTCTGACCAACTGACGTATGTTCCCTTGTGAAATTAATTAACCTG 1389
QY 1381 TTCTGTTTCAT 1391
DB 1390 TTCTGTTTCAT 1400

RESULT 7
US-10-132-829-2

; Sequence 2, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; TITLE OF INVENTION: With vesicle vector
; FILE REFERENCE: 6627-P41170
; CURRENT APPLICATION NUMBER: US/10/132,829
; PRIOR FILING DATE: 2002-04-25
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-132-829-2

Query Match 81.5%; Score 1391; DB 5; Length 2804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAAAGATGATTTCCAGGTTAATTCATTGGAATGAAATTAACAGGCGCTCTAC 60
DB 1414 AATGAAAGATGATTTCCAGGTTAATTCATTGGAATGAAATTAACAGGCGCTCTAC 1473
QY 61 TAACATAATCACTTTCCCATCTTTTGTAGATTGAAATATATACATTCATATGATCT 120
DB 1474 TAACATAATCACTTTCCCATCTTTTGTAGATTGAAATATATACATTCATATGATCT 1533
QY 121 TTTTCTCTTTACAGGGAGAAATTTCAATATTTTACCTGAGCAATGATTAGAAATGAA 180
DB 1354 TTTTCTCTTTACAGGGAGAAATTTCAATATTTTACCTGAGCAATGATTAGAAATGAA 1593
QY 181 CCACAGAGAAATATATATGTTAGAAATTAACATCAATTTCTAAGGCGCCAGCTTGA 240
DB 1594 CCACAGAGAAATATATATGTTAGAAATTAACATCAATTTCTAAGGCGCCAGCTTGA 1653
QY 241 CAAATTTCTGAAATTAATTTCCCACTGTCATCAATCAATCTATAGTTTCCATATAG 300
DB 1654 CAAATTTCTGAAATTAATTTCCCACTGTCATCAATCAATCTATAGTTTCCATATAG 1713
QY 301 CAACTAATCACTCAATTTTCCCTCTTAGAGAGATTCATCTTCCGATCTTTTGTCT 360
DB 1714 CAACTAATCACTCAATTTTCCCTCTTAGAGAGATTCATCTTCCGATCTTTTGTCT 1773
QY 361 TCTCCACCAAAACATCAATGTTTATAGTTTGTATACAGTACAGATCTTTGTCTAC 420

DB 1774 TCTCCACCAAAACATCAATGTTTATAGTTTGTATACAGTACAGATCTTTGTCTAC 1833
QY 421 TCTATCAAAAGGCCAGTACCACTCATGAAAGAAAGAACAGAGATAGTGAAGCTA 480
DB 1834 TCTATCAAAAGGCCAGTACCACTCATGAAAGAAAGAACAGAGATAGTGAAGCTA 1893
QY 481 AAATCAATCAAAACATCACTCTTTTCTCTACCCATTCCTGAATCTTTTACCTTTC 540
DB 1894 AAATCAATCAAAACATCACTCTTTTCTCTACCCATTCCTGAATCTTTTACCTTTC 1953
QY 541 CAAATCCCAATCCCAATCAATGTTTCTCTTCTTACTCCCTCTCCCTTTTACCTTC 600
DB 1954 CAAATCCCAATCCCAATCAATGTTTCTCTTCTTACTCCCTCTCCCTTTTACCTTC 2013
QY 601 CATGTCGTTTAAAGAGATAGGAGATCATCTGTATATCTTGTACACAGTTATA 660
DB 2014 CATGTCGTTTAAAGAGATAGGAGATCATCTGTATATCTTGTACACAGTTATA 2073
QY 661 CATGTCATCAAAACCCAGATCTTCTCTCATATGAGAACTTCTTTCAAGACATAGGGA 720
DB 2074 CATGTCATCAAAACCCAGATCTTCTCTCATATGAGAACTTCTTTCAAGACATAGGGA 2133
QY 721 TGAAGTAAAGTGGCTGAAAAGTTGGGGAAAAGTTTCTTCAAGAGTTAAGTTATTT 780
DB 2134 TGAAGTAAAGTGGCTGAAAAGTTGGGGAAAAGTTTCTTCAAGAGTTAAGTTATTT 2193
QY 781 AT 840
DB 2194 AT 2253
QY 841 TATGCTGTGTGTGACACACACCCATACACATATATATATATATATATATATATATAT 900
DB 2254 TATGCTGTGTGTGACACACACCCATACACATATATATATATATATATATATATATAT 2313
QY 901 AGAGCTGTATGTTATGAGAGTCTGACTAGGCAATGTTTCAAGAGCAAGATTTGAT 960
DB 2314 AGAGCTGTATGTTATGAGAGTCTGACTAGGCAATGTTTCAAGAGCAAGATTTGAT 2373
QY 961 ATCATTTGTAATTAATAAAAGTGAATGACCCAGACATATTTGATCTTTCTTAAATAA 1020
DB 2374 ATCATTTGTAATTAATAAAAGTGAATGACCCAGACATATTTGATCTTTCTTAAATAA 2433
QY 1021 TAAT 1080
DB 2434 TAAT 2493
QY 1081 CTTTGAAGAGATTTCAACAGTGTCTTCAAGAGTCTTCAAGAGCAAGAAAGTTGA 1140
DB 2494 CTTTGAAGAGATTTCAACAGTGTCTTCAAGAGTCTTCAAGAGCAAGAAAGTTGA 2553
QY 1141 AGTGCCTAGACACAGAGACATTAAGTATGATGTCCTTTAACTAGCATACCCGAAATG 1200
DB 2554 AGTGCCTAGACACAGAGACATTAAGTATGATGTCCTTTAACTAGCATACCCGAAATG 2613
QY 1201 GAGAAAGGTGACAGAGGCTCAAAGGCAATAGTCAATTCAGCACTAAGTTGTCT 1260
DB 2614 GAGAAAGGTGACAGAGGCTCAAAGGCAATAGTCAATTCAGCACTAAGTTGTCT 2673
QY 1261 TTTCTGTTTCTGTTTACCAATGAAATTTGATTAATAGTTAACTCTTATCTGTAAT 1320
DB 2674 TTTCTGTTTCTGTTTACCAATGAAATTTGATTAATAGTTAACTCTTATCTGTAAT 2733
QY 1321 CTCTAGAGAGTCTGACCAACTGACGTATGTTCCCTTGTGAAATTAATTAACCTG 1380
DB 2734 CTCTAGAGAGTCTGACCAACTGACGTATGTTCCCTTGTGAAATTAATTAACCTG 2793
QY 1381 TTCTGTTTCAT 1391
DB 2794 TTCTGTTTCAT 2804

RESULT 8
US-10-133-907-2

QY	1	AATGAAAGTGGATTTCCAGGTTAAATTCATATGGAAATGAAATTAACAGGACCTCTCAC	60
Db	1414	AATGAAAGTGGATTTCCAGGTTAAATTCATATGGAAATGAAATTAACAGGACCTCTCAC	1473
QY	61	TAACAAATGACATTTCCCATCTTTGTAGATTTGAAATTAATTAACATTAAGATCAATGCT	120
QY	1474	TAACAAATGACATTTCCCATCTTTGTAGATTTGAAATTAATTAACATTAAGATCAATGCT	1533
QY	121	TTTTCCTCTTAAAGAGGAGAAATTCATATTTTACCTAGCAAAATTTGATTTGAAAAATGAAA	180
Db	1534	TTTTCCTCTTAAAGAGGAGAAATTCATATTTTACCTAGCAAAATTTGATTTGAAAAATGAAA	1593
QY	181	CCACTAAGAGGAATTAATGTGTAGAAATTAACAGTCAATTTCTAAGGCCCAAGCCCTTGA	240
Db	1594	CCACTAAGAGGAATTAATGTGTAGAAATTAACAGTCAATTTCTAAGGCCCAAGCCCTTGA	1653
QY	241	CAAAATGTGAAAGTTAAATTCCTCACTCTGTCCATCAGATACATAAGGTTCTCCACTATGG	300
Db	1654	CAAAATGTGAAAGTTAAATTCCTCACTCTGTCCATCAGATACATAAGGTTCTCCACTATGG	1713
QY	301	CAACTAACTCACTCAATTTTCCCTCTTAGACAGATTCATCTTCCGATCTTTTGGCT	360
Db	1714	CAACTAACTCACTCAATTTTCCCTCTTAGACAGATTCATCTTCCGATCTTTTGGCT	1773
QY	361	TCCTCAACCAAAAATCATCATGTTATTAGTTCTGTATACAGTACAGGATCTTGGTCTAC	420
Db	1774	TCCTCAACCAAAAATCATCATGTTATTAGTTCTGTATACAGTACAGGATCTTGGTCTAC	1833
QY	421	TCATATCAAAAGGCGATGACCACTCATGAAAGAAAGAACAGAGTAGTCTGAGAGGCTTA	480
Db	1834	TCATATCAAAAGGCGATGACCACTCATGAAAGAAAGAACAGAGTAGTCTGAGAGGCTTA	1893
QY	481	AAACTCATCAAAAACATCACTCCCTTTCCCTCAACCCATTCCTCAATCTTTTACCTTTTC	540
Db	1894	AAACTCATCAAAAACATCACTCCCTTTCCCTCAACCCATTCCTCAATCTTTTACCTTTTC	1953
QY	541	CAAAATCCCAATCCCAATCAATGTTTTCCTCTTCTTAATCTCCCTCTCTCCCTTTTACCTTC	600
Db	1954	CAAAATCCCAATCCCAATCAATGTTTTCCTCTTCTTAATCTCCCTCTCTCCCTTTTACCTTC	2013
QY	601	CATGCTGTGTTAAAGAGAGATGGGAGACATCTCTGTATATCTTCTGTACACAGTTATA	660
Db	2014	CATGCTGTGTTAAAGAGAGATGGGAGACATCTCTGTATATCTTCTGTACACAGTTATA	2073
QY	661	CATGCTATATCAAAACCCAGACTTGCTTCATATGAGAGACTTGCTTTCAAAATATAGGGA	720
Db	2074	CATGCTATATCAAAACCCAGACTTGCTTCATATGAGAGACTTGCTTTCAAAATATAGGGA	2133
QY	721	TGAAGTAGAGTGCTGTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTTAAGTATTTT	780

1. **האגודה תפעל כגוף חסר כושר משפטי**

Query Match	81.5%;	Score 1391;	DB 9;	Length 2804;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1391;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
0Y	1	AATGAAAGATGGAATTTCCAGGTTAATTCATTGGAATTGAAATTAACAGGCGCTTCAC	60	

Db 2002 CATGCTCTTAAGAGAGATGGGAGCATATCTGTTATATCTCTGACACAGTATA 2061
Qy 661 CATGCTATCAACCAGACTTGCTCCATAGTGAGACTTCTTTTCAAGACATAGGA 720
Db 2062 CATGCTATCAACCAGACTTGCTCCATAGTGAGACTTCTTTTCAAGACATAGGA 2121
Qy 721 TGAAGTAAAGTGGCCGAAAAGTTTGGGGAAAAGTTCTTTGAGAGATTAATTTT 780
Db 2122 TGAAGTAAAGTGGCCGAAAAGTTTGGGGAAAAGTTCTTTGAGAGATTAATTTT 2181
Qy 781 AT 840
Db 2182 AT 2241
Qy 841 TATGCTGTGTGTAGACACACACGATACACATATATATATATATATATATATATAT 900
Db 2242 TATGCTGTGTGTAGACACACACGATACACATATATATATATATATATATATATAT 2301
Qy 901 AGAGCTTTATGCTTATATAGAGTCTGACATAGGATTTTCAAGAGGCAAGATTGGCAT 960
Db 2302 AGAGCTTTATGCTTATATAGAGTCTGACATAGGATTTTCAAGAGGCAAGATTGGCAT 2361
Qy 961 ATCATTTGTAATTAATAAAGCTGACATTTGACCAATATTTGATCTTTTCAAAAAATA 1020
Db 2362 ATCATTTGTAATTAATAAAGCTGACATTTGACCAATATTTGATCTTTTCAAAAAATA 2421
Qy 1021 TATATATATATGCTAAACAGAAAGAGAAACCGTTGCTTTCATCTACAGTATAGAGA 1080
Db 2422 TATATATATATGCTAAACAGAAAGAGAAACCGTTGCTTTCATCTACAGTATAGAGA 2481
Qy 1081 CTTTGAGAGAAATTCACAGTGTCTTACAGAGTTCAGAGGCAAGCAAGAGTTGA 1140
Db 2482 CTTTGAGAGAAATTCACAGTGTCTTACAGAGTTCAGAGGCAAGCAAGAGTTGA 2541
Qy 1141 AGTTGCTTGAACAGAGGACATATATATATATATATATATATATATATATATATAT 1200
Db 2542 AGTTGCTTGAACAGAGGACATATATATATATATATATATATATATATATATATAT 2601
Qy 1201 GAGAAAGGTGACAGAGGCTCAAGGCAATATATATATATATATATATATATATAT 1260
Db 2602 GAGAAAGGTGACAGAGGCTCAAGGCAATATATATATATATATATATATATATAT 2661
Qy 1261 TTTTGTGTTGCTTCCATGAGAAATTTGATATATATATATATATATATATATATAT 1320
Db 2662 TTTTGTGTTGCTTCCATGAGAAATTTGATATATATATATATATATATATATATAT 2721
Qy 1321 CTTCAGAGAGTGTGACCAACATGATATATATATATATATATATATATATATATAT 1380
Db 2722 CTTCAGAGAGTGTGACCAACATGATATATATATATATATATATATATATATAT 2781
Qy 1381 TTTGCTTTCAT 1391
Db 2782 TTTGCTTTCAT 2792

RESULT 12
US-10-349-858-16
; Sequence 16, Application US/10349858
; Publication No. US20030220247A1
; GENERAL INFORMATION:
; APPLICANT: The Children's Hospital of Philadelphia
; APPLICANT: HIGH, KATHERINE A.
; APPLICANT: CAMIRE, RODNEY M.
; APPLICANT: LARSON, PETER J.
; APPLICANT: STAFFORD, DARREL W.
; TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT C
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: 018743-0301425
; CURRENT APPLICATION NUMBER: US/10/349,858
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 09/526,947
; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 60/124,609
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-858-16

Query Match 80.7%; Score 1377; DB 6; Length 2773;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 2; Gaps 1;
Matches 1389; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

1 AATGAAAGATGATTTCCAGAGTTAATTCATTTGATGAAATTAATTAAGGGCTCTTAC 60
Db 1385 AATGAAAGATGATTTCCAGAGTTAATTCATTTGATGAAATTAATTAAGGGCTCTTAC 1444
Qy 61 TAACTATCACTTCCATCTTTTGTATGATTTGAATTAATTAATTAATTAATTAATTA 120
Db 1445 TAACTATCACTTCCATCTTTTGTATGATTTGAATTAATTAATTAATTAATTAATTA 1504
Qy 121 TTTTCTCTTTACAGGGAGATTTCAATTTTACCTGAGCAATTTGATTAAGAAATGGA 180
Db 1505 TTTTCTCTTTACAGGGAGATTTCAATTTTACCTGAGCAATTTGATTAAGAAATGGA 1564
Qy 181 CCAGTAAAGATTAATATGTTAGAAATTAAGATTAATTAATTAATTAATTAATTAATTA 240
Db 1565 CCAGTAAAGATTAATATGTTAGAAATTAAGATTAATTAATTAATTAATTAATTAATTA 1624
Qy 241 CAATAATGTAAGTTAATTTCTCACTGTGTCAATCAATATATATATATATATATATAT 300
Db 1625 CAATAATGTAAGTTAATTTCTCACTGTGTCAATCAATATATATATATATATATATAT 1684
Qy 301 CAATTAATCACTGAATTTTCTCTTCCAGAGATTCATCTTCCAGATCTTCTTGTCT 360
Db 1685 CAATTAATCACTGAATTTTCTCTTCCAGAGATTCATCTTCCAGATCTTCTTGTCT 1744
Qy 361 TCTCCAAACCAAAATCAATGTTTATATATATATATATATATATATATATATATATAT 420
Db 1745 TCTCCAAACCAAAATCAATGTTTATATATATATATATATATATATATATATATATAT 1804
Qy 421 TCTATCAAGGCGATGACCACTCATGAGAAAGAAACAGAGATGATGAGAGGCTA 480
Db 1805 TCTATCAAGGCGATGACCACTCATGAGAAAGAAACAGAGATGATGAGAGGCTA 1864
Qy 481 AAACATCAAAACCACTACCTCTTCTCACTTCTCACTTCTCACTTCTTCTTCTTCTTCT 540
Db 1865 AAACATCAAAACCACTACCTCTTCTCACTTCTCACTTCTCACTTCTTCTTCTTCTTCT 1924
Qy 541 CAATCCCAATCCCAATCAATGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
Db 1925 CAATCCCAATCCCAATCAATGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1984
Qy 601 CATGCTGTTTAAAGAGATGGGAGATCAATCTGTTATATATATATATATATATATATAT 660
Db 1985 CATGCTGTTTAAAGAGATGGGAGATCAATCTGTTATATATATATATATATATATATAT 2044
Qy 661 CATGCTATCAACCAGACTTGCTCCATAGTGAGACTTCTTTTCAAGACATAGGA 720
Db 2045 CATGCTATCAACCAGACTTGCTCCATAGTGAGACTTCTTTTCAAGACATAGGA 2104
Qy 721 TGAAGTAAAGTGGCCGAAAAGTTTGGGGAAAAGTTCTTTGAGAGATTAATTTT 780
Db 2105 TGAAGTAAAGTGGCCGAAAAGTTTGGGGAAAAGTTCTTTGAGAGATTAATTTT 2164
Qy 781 AT 840
Db 2165 AT 2224
Qy 841 TATGCTGTGTGTAGACACACACGATACACATATATATATATATATATATATATATAT 900
Db 2225 TATGCTGTGTGTAGACACACACGATACACATATATATATATATATATATATATATATAT 2284

QY 901 AGAGCTGTATGTTATGAGGCTGCTAGCTAGCATATTTCAAGAGGCAAGATTGGCAT 960
DB 2285 AGAGCTGTATGTTATGAGGCTGCTAGGATATTTCAAGAGGCAAGATTGGCAT 2344
QY 961 ATCATTTGTACTTAAAGAGGCTGATTTGACCCAGACATATTTGACTCTTTCTTAAATA 1020
DB 2345 ATCATTTGTACTTAAAGAGGCTGATTTGACCCAGACATATTTGACTCTTTCTTAAATA 2402
QY 1021 TAATATAATGCTTAAAGAGGCAAGAGGCTGCTGCTTGAATCTAGAGCTAGTAGAGA 1080
DB 2403 TAATATAATGCTTAAAGAGGCAAGAGGCTGCTGCTTGAATCTAGAGCTAGTAGAGA 2462
QY 1081 CTTTGAAGAGAAATTTCAACAGTGTCTTCAAGAGCTTCAAGAGGCAAGAGGCTTGA 1140
DB 2463 CTTTGAAGAGAAATTTCAACAGTGTCTTCAAGAGCTTCAAGAGGCAAGAGGCTTGA 2522
QY 1141 AGTTGCTTGAAGAGGCAAGAGGCTTCAAGAGCTTCAAGAGGCTTCAAGAGGCTTGA 1200
DB 2523 AGTTGCTTGAAGAGGCAAGAGGCTTCAAGAGCTTCAAGAGGCTTCAAGAGGCTTGA 2582
QY 1201 GAGAGGCTGAGAGGCTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 1260
DB 2583 GAGAGGCTGAGAGGCTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 2642
QY 1261 TTTTGGTTTGGTTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 1320
DB 2643 TTTTGGTTTGGTTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 2702
QY 1321 CTTTGAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 1380
DB 2703 CTTTGAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 2762
QY 1381 TTTTGGTTTCAAT 1391
DB 2763 TTTTGGTTTCAAT 2773

RESULT 13
US-10-741-600-3
Sequence 3, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGIL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001499
CURRENT APPLICATION NUMBER: US/10741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 7397
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2728
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2728)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-3

Query Match 80.6%; Score 1376.6; DB 8; Length 2728;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1388; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 ATGGAAGATGATTTCCAGGTTAATTTCAATTTGAAATTAAGAGGCTTCCAC 60
DB 1340 ATGGAAGATGATTTCCAGGTTAATTTCAATTTGAAATTAAGAGGCTTCCAC 1399
QY 61 TAACTAATCACTTTCCATCTTTTGTAGATTGAAATATATACATTTGATCATTTGCT 120
DB 1400 TAACTAATCACTTTCCATCTTTTGTAGATTGAAATATATACATTTGATCATTTGCT 1459

QY 121 TTTTCTTTTCAAGGAGGAAATTTCAATTTTACCTGAGCAATTTGATTAAGAAATGAA 180
DB 1460 TTTTCTTTTCAAGGAGGAAATTTCAATTTTACCTGAGCAATTTGATTAAGAAATGAA 1519
QY 181 CCACTAGAGGAATTAATTTGTAGAGAAATTAAGATCAATTTCTTAAGGGCCAGGCTTGA 240
DB 1520 CCACTAGAGGAATTAATTTGTAGAGAAATTAAGATCAATTTCTTAAGGGCCAGGCTTGA 1579
QY 241 CAAATTTGAGAGTAAATTTCCAGCTGCTGCTCAATCAATCAATCAATCAATCAATCAAT 300
DB 1580 CAAATTTGAGAGTAAATTTCCAGCTGCTGCTCAATCAATCAATCAATCAATCAATCAAT 1639
QY 301 CAATTAATCAATCAATTTTCCCTTCTTGAAGCAATTCATCTTCCGATCTTCTTCT 360
DB 1640 CAATTAATCAATCAATTTTCCCTTCTTGAAGCAATTCATCTTCCGATCTTCTTCT 1699
QY 361 TCTCAACCAAAACATCAATTTTATTTATTTGTATTTGTATTTGTATTTGTATTTGTAT 420
DB 1700 TCTCAACCAAAACATCAATTTTATTTATTTGTATTTGTATTTGTATTTGTATTTGTAT 1759
QY 421 TCTATCAAGGCGAGTACACATCAATGAGAAAGAACAGAGAGTGTAGAGGCTA 480
DB 1760 TCTATCAAGGCGAGTACACATCAATGAGAAAGAACAGAGAGTGTAGAGGCTA 1819
QY 481 AAATCAATCAAAACATCAATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
DB 1820 AAATCAATCAAAACATCAATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1879
QY 541 CAAATCCCAATCCCAATCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
DB 1880 CAAATCCCAATCCCAATCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1939
QY 601 CATGCTGTTAAAGAGAGAGTGGAGAGCATCATCTGTATTAATCTTGTATACAGTTATA 660
DB 1940 CATGCTGTTAAAGAGAGAGTGGAGAGCATCATCTGTATTAATCTTGTATACAGTTATA 1999
QY 721 TGAAGTAAAGGCTGAAAGGTTTGGGGGAAAGTTCTTCAAGAGGTTAAGTTATTT 780
DB 2000 TGAAGTAAAGGCTGAAAGGTTTGGGGGAAAGTTCTTCAAGAGGTTAAGTTATTT 2059
QY 781 AT 840
DB 2120 AT 2177
QY 841 TATGCTGTGTGTAGACACAGGATACACATATATATATATATATATATATATATATAT 900
DB 2178 TATGCTGTGTGTGTAGACACAGGATACACATATATATATATATATATATATATATAT 2237
QY 901 AGAGCTGTATGTTATGAGAGGCTGATCTAGGATGATTTCAAGAGGCAAGATTGGCAT 960
DB 2238 AGAGCTGTATGTTATGAGAGGCTGATCTAGGATGATTTCAAGAGGCAAGATTGGCAT 2297
QY 961 ATCATTTGTAATTAAGAGGCTGATTTGACCCAGACATATTTGATTTGATTTGATTTGAT 1020
DB 2298 ATCATTTGTAATTAAGAGGCTGATTTGACCCAGACATATTTGATTTGATTTGATTTGAT 2357
QY 1021 TAATATAATGCTTAAAGAGGCAAGAGGCTGCTGCTTGAATCTAGAGCTAGTAGAGA 1080
DB 2358 TAATATAATGCTTAAAGAGGCAAGAGGCTGCTGCTTGAATCTAGAGCTAGTAGAGA 2417
QY 1081 CTTTGAAGAGAAATTTCAACAGTGTCTTCAAGAGCTTCAAGAGGCTTCAAGAGGCTTGA 1140
DB 2418 CTTTGAAGAGAAATTTCAACAGTGTCTTCAAGAGCTTCAAGAGGCTTCAAGAGGCTTGA 2477
QY 1141 AGTTGCTTGAAGAGGCAAGAGGCTTCAAGAGCTTCAAGAGGCTTCAAGAGGCTTGA 1200
DB 2478 AGTTGCTTGAAGAGGCAAGAGGCTTCAAGAGCTTCAAGAGGCTTCAAGAGGCTTGA 2537
QY 1201 GAGAGGCTGAGAGGCTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTGA 1260

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Db      2538 GAGAGAGGTGAGAGAGGTGCAAGAGCAATGATTCAGATCAGGCACTAAGTGTCT 2597
Qy      1261 TTCTGCTTTCGTTGTTCCAGCAGCAATTTGATTAATGTTATCTTCTATCTTGAT 1320
Db      2598 TTCTGCTTTCGTTGTTCCAGCAGCAATTTGATTAATGTTATCTTCTATCTTGAT 2657
Qy      1321 CTCTTAAGAGTTTCTGAGCACTGAGAGTATGTTCCCTTGTGAATTAATAACTGGTG 1380
Db      2658 CTCTTAAGAGTTTCTGAGCACTGAGAGTATGTTCCCTTGTGAATTAATAACTGGTG 2717
Qy      1381 TTCTGTTTCAT 1391
Db      2718 TTCTGTTTCAT 2728

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RESULT 14

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US-10-741-600-1
; Sequence 1, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2771)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-1

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Query Match 80.6%; Score 1376.6; DB 8; Length 2771;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1388; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

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Qy      1 AATGAAAGATGATTTCCAGGTTAATTCATTGAAATGAAATTAACAGGCGCTCTCAC 60
Db      1383 AATGAAAGATGATTTCCAGGTTAATTCATTGAAATGAAATTAACAGGCGCTCTCAC 1442
Qy      61 TAACTAATCACTTCCATCTTTGTTAGATTGAAATTAATTAATCAATTCATGATCT 120
Db      1443 TAACTAATCACTTCCATCTTTGTTAGATTGAAATTAATTAATCAATTCATGATCT 1502
Qy      121 TTTTCTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTAGAAATGAA 180
Db      1503 TTTTCTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTAGAAATGAA 1562
Qy      1503 TTTTCTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTTAGAAATGAA 1622
Db      181 CCACAGAGGAATTAATGTTAGAAATTAACATCTTCTAAGGCGCCAGCCCTTGA 240
Qy      1563 CCACAGAGGAATTAATGTTAGAAATTAACATCTTCTAAGGCGCCAGCCCTTGA 1622
Db      241 CAAATTTGAGAGTAAATTTCTCACTCTGTCATCAGATTAATGTTTCTCACTATG 300
Qy      1623 CAAATTTGAGAGTAAATTTCTCACTCTGTCATCAGATTAATGTTTCTCACTATG 1682
Db      301 CAATTAATCACTCAATTTTCCCTCTTAAGCAGATTCATTTCCCATCTTCTTGCT 360
Qy      1683 CAATTAATCACTCAATTTTCCCTCTTAAGCAGATTCATTTCCCATCTTCTTGCT 1742
Db      361 TCTCAACCAAAACATCATGTTTATTTAGTTCTGTATACAGTACAGATCTTGTCTAC 420
Qy      1743 TCTCAACCAAAACATCATGTTTATTTAGTTCTGTATACAGTACAGATCTTGTCTAC 1802
Db      421 TCTATCAGAGCCAGTACCACTCATGAGAAAGAACAGAGAGTACTGAGAGCTA 480

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Db      1803 TCTATCAGAGCCAGTACCACTCATGAGAAAGAACAGAGAGTACTGAGAGCTA 1862
Qy      481 AACTCATCAAAAACACTACTCTTTCTCTCACTTCCCTCAATCTTTACCTTTTC 540
Db      1863 AACTCATCAAAAACACTACTCTTTCTCTCACTTCCCTCAATCTTTACCTTTTC 1922
Qy      541 CAAATCCCAATCCCAATCAATGTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 600
Db      1923 CAAATCCCAATCCCAATCAATGTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 1982
Qy      601 CAGGTGCTTAAGAGAGATGAGAGATCAATCTGTATTAATCTTGTATACAGATTATA 660
Db      1983 CAGGTGCTTAAGAGAGATGAGAGATCAATCTGTATTAATCTTGTATACAGATTATA 2042
Qy      661 CATGCTATCAAAACCCAGACTTGTCTCAATAGAGAGATGCTTTTCAGAACTAGGGA 720
Db      2043 CATGCTATCAAAACCCAGACTTGTCTCAATAGAGAGATGCTTTTCAGAACTAGGGA 2102
Qy      721 TGAAGTAAAGTCCCTGAAAGATTGGGGGAAAGTTTCTTTCAGAGAGTTAAAGTTATTT 780
Db      2103 TGAAGTAAAGTCCCTGAAAGATTGGGGGAAAGTTTCTTTCAGAGAGTTAAAGTTATTT 2162
Qy      781 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
Db      2163 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
Qy      841 TATGCGTGTGTGTAGACACACAGCCATACACATATATATGAGAGCAATTAAGCAATCTTA 900
Db      2221 TATGCGTGTGTGTAGACACACAGCCATACACATATATATGAGAGCAATTAAGCAATCTTA 2280
Qy      901 AGAGCTGTATGTATATGAGAGTCTGACTAGGCAATTTTACAGAGGCAAGATTGGAT 960
Db      2281 AGAGCTGTATGTATATGAGAGTCTGACTAGGCAATTTTACAGAGGCAAGATTGGAT 2340
Qy      961 ATCATTTGAATTAATAAAGAGTGAATGAGCCAGACATATGTACTCTTTTAAATAATA 1020
Db      2341 ATCATTTGAATTAATAAAGAGTGAATGAGCCAGACATATGTACTCTTTTAAATAATA 2400
Qy      1021 TAATTAATTAATCTTAACAGAAAGAGAAAGAAAGCCGTTGTTGCAATCTACAGCTAGTAGA 1080
Db      2401 TAATTAATTAATCTTAACAGAAAGAGAAAGAAAGCCGTTGTTGCAATCTACAGCTAGTAGA 2460
Qy      1081 CTTTGAAGAGATTCACAGATGTCTTTCAGAGAGTCTTTCAGAGCCAGAAAGATTGA 1140
Db      2461 CTTTGAAGAGATTCACAGATGTCTTTCAGAGAGTCTTTCAGAGCCAGAAAGATTGA 2520
Qy      1141 AGTTGCCAGACAGAGACATAGATCATGTCTCCTTTAATAGCATACCCGGAATG 1200
Db      2521 AGTTGCCAGACAGAGACATAGATCATGTCTCCTTTAATAGCATACCCGGAATG 2580
Qy      1201 GAGAAAGGTGAGAGAGGCTCAAGAGCATTAATTCATTCAGCCAACTAAGTTGTCT 1260
Db      2581 GAGAAAGGTGAGAGAGGCTCAAGAGCATTAATTCATTCAGCCAACTAAGTTGTCT 2640
Qy      1261 TTTCTGTTTGTGTTCACATGAGAACTTTTGAATTAATGTTATCTTCTATCTTGAT 1320
Db      2641 TTTCTGTTTGTGTTCACATGAGAACTTTTGAATTAATGTTATCTTCTATCTTGAT 2700
Qy      1321 CTCTTAAGAGTTTCTGAGCACTGAGAGTATGTTCCCTTGTGAATTAATAACTGGTG 1380
Db      2701 CTCTTAAGAGTTTCTGAGCACTGAGAGTATGTTCCCTTGTGAATTAATAACTGGTG 2760
Qy      1381 TTCTGTTTCAT 1391
Db      2761 TTCTGTTTCAT 2771

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RESULT 15

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US-10-741-600-2
; Sequence 2, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

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QY 241 CAAATGTGAGTAAATCTCACTGTCATCAGATCTAGTGTCTCACTAGG 300
 Db 34573 CAAATGTGAGTAAATCTCACTGTCATCAGATCTAGTGTCTCACTAGG 34632
 QY 301 CAACTACTCACTCAATTTCTCTCTAGAGCATTCATCTTCCCATCTTCTTCT 360
 Db 34633 CAACTACTCACTCAATTTCTCTCTAGAGCATTCATCTTCCCATCTTCTTCT 34692
 QY 361 TCTCCAAACCAAACTCAATGTTTATAGTCTGTATCAGTACGAGATCTTGGTCTAC 420
 Db 34693 TCTCCAAACCAAACTCAATGTTTATAGTCTGTATCAGTACGAGATCTTGGTCTAC 34752
 QY 421 TCTATCAACAGGCGATACCACTCACTGAGAAAGAACAGAGAGTACTGAGAGCTA 480
 Db 34753 TCTATCAACAGGCGATACCACTCACTGAGAAAGAACAGAGAGTACTGAGAGCTA 34812
 QY 481 AAATCTCAAAACCACTACTCTCTTCTCTACCTTATCTCTCATCTTCTTCTTCT 540
 Db 34813 AAATCTCAAAACCACTACTCTCTTCTCTACCTTATCTCTCATCTTCTTCTTCT 34872
 QY 541 CAAATCCCAATCCCAATCACTTCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCT 600
 Db 34873 CAAATCCCAATCCCAATCACTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 34932
 QY 601 CATGCTCGTTAAGAGAGATGGGAGAGCATCTCTGTTATATCTCTGTACACAGTTATA 660
 Db 34933 CATGCTCGTTAAGAGAGATGGGAGAGCATCTCTGTTATATCTCTGTACACAGTTATA 34992
 QY 661 CATGCTCTACAAACCCAGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 Db 34993 CATGCTCTACAAACCCAGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35052
 QY 721 TGAAGTAAAGGCGCTGAAAGATTGGGGGAAAGATTCTTCTCAGAGAGTTAAGTTATTT 780
 Db 35053 TGAAGTAAAGGCGCTGAAAGATTGGGGGAAAGATTCTTCTCAGAGAGTTAAGTTATTT 35112
 QY 781 AT 840
 Db 35113 AT 35172
 QY 841 TATGCGGTGTGTGTGACACACACGATATACACATATATATATATATATATATATAT 900
 Db 35173 TATGCGGTGTGTGTGACACACACGATATACACATATATATATATATATATATATAT 35232
 QY 901 AGAGCTGTATGTGTATGAGAGTCTGACTAGGAGTATTTCAAGAGGCAAGATTGGCAT 960
 Db 35233 AGAGCTGTATGTGTATGAGAGTCTGACTAGGAGTATTTCAAGAGGCAAGATTGGCAT 35292
 QY 961 ATCATTTGTAATTAATAAAGCTGACATTTGACCCAGACATATTTGTAATTTCTTAATAATA 1020
 Db 35293 ATCATTTGTAATTAATAAAGCTGACATTTGACCCAGACATATTTGTAATTTCTTAATAATA 35352
 QY 1021 TAAATATATATGCTTAACGAAAGAGAGAACCTGCTCTTCTCAATCTCACTAGTATAGA 1080
 Db 35353 TAAATATATATGCTTAACGAAAGAGAGAACCTGCTCTTCTCAATCTCACTAGTATAGA 35412
 QY 1081 CTTTGAAGAGAAATTTCAACAGTGTCTTCTCAGAGTGTTCAGAGCCAAAGAGAGTTGA 1140
 Db 35413 CTTTGAAGAGAAATTTCAACAGTGTCTTCTCAGAGTGTTCAGAGCCAAAGAGAGTTGA 35472
 QY 1141 AGTTGCTTAAGACGAGAGCAATTAATGATCTCTCTTAACTAGCATACCCGAAAGTG 1200
 Db 35473 AGTTGCTTAAGACGAGAGCAATTAATGATCTCTCTTAACTAGCATACCCGAAAGTG 35532
 QY 1201 GAGAGGAGTGCAGAGGCTCAAGAGCAATAGTATTTCCATTCAGCCAACTAAGTTGCTT 1260
 Db 35533 GAGAGGAGTGCAGAGGCTCAAGAGCAATAGTATTTCCATTCAGCCAACTAAGTTGCTT 35592
 QY 1261 TTTCTGTGTTTGTGTTCACATGGAACATTTGTAATAGTTAATCTTCTCATCTTGAAT 1320
 Db 35593 TTTCTGTGTTTGTGTTCACATGGAACATTTGTAATAGTTAATCTTCTCATCTTGAAT 35652

QY 1321 CTTCTAGAGAGTCTGACCAACTGACGTATGTTTCCCTTGTGAAATTAATAACGTGTG 1380
 Db 35653 CTTCTAGAGAGTCTGACCAACTGACGTATGTTTCCCTTGTGAAATTAATAACGTGTG 35712
 QY 1381 TTTCTGTTTCAATCTTGGCTTTTGTGAGATTCATTTGATGATTCAGTCAACCTGATTT 1440
 Db 35713 TTTCTGTTTCAATCTTGGCTTTTGTGAGATTCATTTGATGATTCAGTCAACCTGATTT 35772
 QY 1441 TGATGATGCAATGGGACTACTGACAAATCACTGACCCCTGCAAGCTGCTGCTCTCC 1500
 Db 35773 TGATGATGCAATGGGACTACTGACAAATCACTGACCCCTGCAAGCTGCTGCTCTCC 35832
 QY 1501 TGCCCAACCTCAACCCCAAGAGGCTCACTCTTGTAGTCTTGTAGTTCTTTAGTGC 1560
 Db 35833 TGCCCAACCTCAACCCCAAGAGGCTCACTCTTGTAGTCTTGTAGTTCTTTAGTGC 35892
 QY 1561 AATATATTTTGTGTTGCAATATATATATATATATATATATATATATATATATATAT 1620
 Db 35893 AATATATTTTGTGTTGCAATATATATATATATATATATATATATATATATATATAT 35952
 QY 1621 GCCCAGTGCACAGCCTATATATCCAGCACTTCTGAGGCAAGTGGCGATCACT 1680
 Db 35953 GCCCAGTGCACAGCCTATATATCCAGCACTTCTGAGGCAAGTGGCGATCACT 36012
 QY 1681 GAGGTAGAGATTTCAGGCCAAGCT 1705
 Db 36013 GAGGTAGAGATTTCAGGCCAAGCT 36037

RESULT 2
 US-11-129-861-3
 ; Sequence 3, Application US/11129861
 ; Publication NO. US20060031956A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kurachi, Suniko
 ; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
 ; FILE REFERENCE: UM-03603
 ; CURRENT FILING DATE: 2005-05-16
 ; PRIOR APPLICATION NUMBER: US/09/328,925
 ; PRIOR FILING DATE: 1999-06-09
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1273
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-11-129-861-3

Query Match 74.6%; Score 1273; DB 11; Length 1273;
 Best Local Similarity 100.0%; Pred. No. 1.8e-61;
 Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GGCCTCTCACTAATCACTTCCCATCTTGTGTTAGTTGAATATATATATATATAT 110
 Db 1 GGCCTCTCACTAATCACTTCCCATCTTGTGTTAGTTGAATATATATATATATATAT 60
 QY 111 GATCATTTGCTTTTCTCTTACAGGGAGAAATTTCAATTTTACCTGAGCAATTTGATTA 170
 Db 61 GATCATTTGCTTTTCTCTTACAGGGAGAAATTTCAATTTTACCTGAGCAATTTGATTA 120
 QY 171 GAAATGGAACCACTAGAGAAATATATATATATATATATATATATATATATATATATAT 230
 Db 121 GAAATGGAACCACTAGAGAAATATATATATATATATATATATATATATATATATATAT 180
 QY 231 CAGCCCTTGCAAAATTTGGAAGTTAATTTCTCATCTGTCTCATATAGATATATATATAT 290
 Db 181 CAGCCCTTGCAAAATTTGGAAGTTAATTTCTCATCTGTCTCATATAGATATATATATAT 240
 QY 291 TCCACTATGGAACCTAATCACTCAATTTTCCCTCTTACAGCATTCATCTCCGAT 350

241 TCCACTATGGAAGTAACCTCACTCAATTTCCCTCTTAGCAGACATTCATCTCCCAT 300
QY CTTCTTTGCTCTTCCAAACCAAAACATGTTTATGTTCTGTATACAGTACGAGATC 410
Db CTTCTTTGCTCTTCCAAACCAAAACATGTTTATGTTCTGTATACAGTACGAGATC 360
QY TTTGGTCTACTCTATCAGAGGCGAGTACCACTCATGAGAGAGAAACAGAGAGTAC 470
Db TTTGGTCTACTCTATCAGAGGCGAGTACCACTCATGAGAGAGAAACAGAGAGTAC 420
QY TGAAGGCTAAAACTCATCAAAAACATCACTCTCTTCTCTCTCTCTCTCTCTCTCT 530
Db TGAAGGCTAAAACTCATCAAAAACATCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 590
Db TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
QY TTTTACCTCTCAATGCTTAAAGAGAGATGGAGAGATCACTCTCTCTCTCTCTCTCT 650
Db TTTTACCTCTCAATGCTTAAAGAGAGATGGAGAGATCACTCTCTCTCTCTCTCTCT 540
QY CACAGTTATACATGCTATCAAAACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db CACAGTTATACATGCTATCAAAACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY AACATGAGAGAGAACTAAGTGGCTGAAAGAGTGGGGGAAAGTGGCTGAGAGAT 770
Db AACATGAGAGAGAACTAAGTGGCTGAAAGAGTGGGGGAAAGTGGCTGAGAGAT 720
QY AACATGAGAGAGAACTAAGTGGCTGAAAGAGTGGGGGAAAGTGGCTGAGAGAT 830
Db AACATGAGAGAGAACTAAGTGGCTGAAAGAGTGGGGGAAAGTGGCTGAGAGAT 780
QY TGT 890
Db TGT 840
QY AGCATTCTTAAGAGCTGT 950
Db AGCATTCTTAAGAGCTGT 900
QY AGATTGGCATATCATTTGTAATTAAGTCAATTTGATCCAGATATTTGATCTCTT 1010
Db AGATTGGCATATCATTTGTAATTAAGTCAATTTGATCCAGATATTTGATCTCTT 960
QY CTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1070
Db CTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
QY CTAAGTAGAGACTTTAGAGAGAAATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1130
Db CTAAGTAGAGACTTTAGAGAGAAATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
QY AAGAAGTGAAGTCTAGACAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1190
Db AAGAAGTGAAGTCTAGACAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1140
QY CCCCAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1250
Db CCCCAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY AAGTGTCTCTTTCTGT 1310
Db AAGTGTCTCTTTCTGT 1260
QY TATCTTGAATCTT 1323
Db TATCTTGAATCTT 1273

; Sequence 83, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: Use thereof
; CURRENT APPLICATION NUMBER: US/11/129,861
; PRIORITY FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/328,925
; PRIORITY FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO: 83
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-129-861-83

Query Match 74.5%; Score 1272; DB 11; Length 1272;
Best Local Similarity 100.0%; Pred. No. 2,1e-61;
Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 GCTCTCACTACTAATCACTCTTCCATCTTTGTGATTTGAATATATACATTTATG 111
Db 1 GCTCTCACTACTAATCACTCTTCCATCTTTGTGATTTGAATATATACATTTATG 60
QY 112 ATCAATGCTTTTCTCTTTACAGGGGAGATTTCAATTTTACCGAGAAATGATAG 171
Db 61 ATCAATGCTTTTCTCTTTACAGGGGAGATTTCAATTTTACCGAGAAATGATAG 120
QY 172 AAAATGGAACCACTAGAGGAATATATATGTTAGAAATTCAGTATTTTCAAGGGCC 231
Db 121 AAAATGGAACCACTAGAGGAATATATATGTTAGAAATTCAGTATTTTCAAGGGCC 180
QY 232 AGCCTTGACAAATTTGAGATTAATTTCACTGTGTCATAGATCTAGTCTT 291
Db 181 AGCCTTGACAAATTTGAGATTAATTTCACTGTGTCATAGATCTAGTCTT 240
QY 292 CCACTAGGCACTACTCATCTTCCCTCTCTTACGAGCATTCATCTCCGATC 351
Db 241 CCACTAGGCACTACTCATCTTCCCTCTCTTACGAGCATTCATCTCCGATC 300
QY 352 TTTCTTGTCTTCCAAACCAATCATGTTTATGTTTCTGTATACAGTACATCT 411
Db 301 TTTCTTGTCTTCCAAACCAATCATGTTTATGTTTCTGTATACAGTACATCT 360
QY 412 TTGGTCTACTATCAGAGGCGAGTACCACTCATGAGAGAGAAACAGAGAGTACT 471
Db 361 TTGGTCTACTATCAGAGGCGAGTACCACTCATGAGAGAGAAACAGAGAGTACT 420
QY 472 GAGAGGCTAAATCTCATTAATAAATCACTCTCTTCTCTACCTATTCCTCATCTT 531
Db 421 GAGAGGCTAAATCTCATTAATAAATCACTCTCTTCTCTACCTATTCCTCATCTT 480
QY 532 TACCTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 591
Db 481 TACCTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
QY 592 TTTACCTCTCAATGCTTAAAGAGAGATGGAGAGATCACTCTCTCTCTCTCTCT 651
Db 541 TTTACCTCTCAATGCTTAAAGAGAGATGGAGAGATCACTCTCTCTCTCTCTCT 600
QY 652 AAGTATATACATGCTATCAAAACCAAGCTTGTCTCTCTCTCTCTCTCTCTCTCT 711
Db 601 AAGTATATACATGCTATCAAAACCAAGCTTGTCTCTCTCTCTCTCTCTCTCTCT 660
QY 712 ACATAGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 771
Db 661 ACATAGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

[illegible]

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RESULT 4
US-11-129-861-76
? Sequence 76, Application US/11129861
? Publication No. US20060031956A1
? GENERAL INFORMATION:
? APPLICANT: Kurachi, Kotoku
? APPLICANT: Kurachi, Sumiko
? TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
? TITLE OF INVENTION: Use Thereof
? FILE REFERENCE: UM-03603
? CURRENT APPLICATION NUMBER: US/11/129,861
? CURRENT FILING DATE: 2005-05-16
? PRIOR APPLICATION NUMBER: US/09/328,925
? PRIOR FILING DATE: 1999-06-09
? NUMBER OF SEQ ID NOS: 84
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 76
? LENGTH: 1273
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-129-861-76

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Query Match	Similarity	Score	1271.4;	DB 11;	Length	1273;
Beet Local	99.9%;	Pred.	No. 2.2e-61;			
Matches	1272;	Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;

QY	51	GGCCTCTCACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCAT	110
cb	1	GGCCTCTGACATCACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCAT	60

Oy		111	GATCATTCCTTTTCTTTACTTTACAGGGGAAATTTCATATTTTAACCGAGCAAAATGTATTA	170
Dd		61	GATCATTCCTTTTCTTTTCTTTACAGGGGAAATTTCAATTTTACCAGCAAAATGTATTA	120
Oy		171	GAAAAATGAACAACACTAGAAGAAATATATATGTGTAGAAATTAACAAGTCTTCTTAAGGGCC	230
Dd		121	GAAAAATGAACAACACTAGAAGAAATATATATGTGTAGAAATTAACAAGTCTTCTTAAGGGCC	180
Oy		231	CAGCCTTGACAAAATGTGAAGTTAATTCTCACCTGTGCATCAGATCTATGTTTTG	290
Dd		181	CAGCCTTGACAAAATGTGAAGTTAATTCTCACCTGTGCATCAGATCTATGTTTTG	240
Oy		291	TCCACTAATGGCAACTATCACTCACTCAATTTTCCCTCCTTAGAGCAATTCATCTTCCCAGT	350
Dd		241	TCCACTAATGGCAACTATCACTCACTCAATTTTCCCTCCTTAGAGCAATTCATCTTCCCAGT	300
Oy		351	CTTCTTGTGCTTCTCCAACCAAAACATCAATGTTTATTAATTTCTGTATACAGTACAGATC	410
Dd		301	CTTCTTGTGCTTCTCCAACCAAAACATCAATGTTTATTAATTTCTGTATACAGTACAGATC	360
Oy		411	TTTGGTCTACTATATCAAGGCCGTACCACTCATAGAAAGAAACAAGAGTATGC	470
Dd		361	TTTGGTCTACTATATCAAGGCCGTACCACTCATAGAAAGAAACAAGAGTATGC	420
Oy		471	TGAGAGGGCTAAAACATCAATAAAAACATCACTCCTTTTCCCTAACCTATTTCTCATCTT	530
Dd		421	TGAGAGGGCTAAAACATCAATAAAAACATCACTCCTTTTCCCTAACCTATTTCTCATCTT	480
Oy		531	TTACCTTTTCCAAATCCCAATCCCAATCAAGTTTTTCTCTTTCTTACTCCTCTCTCCC	590
Dd		481	TTACCTTTTCCAAATCCCAATCCCAATCAAGTTTTTCTCTTTCTTACTCCTCTCTCCC	540
Oy		591	TTTTACCTTCCATATGGTGTGTTAAAGAGAGATGGGGAGATCATCTCTGTATCTCTGTGA	650
Dd		541	TTTTACCTTCCATATGGTGTGTTAAAGAGAGATGGGGAGATCATCTCTGTATCTCTGTGA	600
Oy		651	CACAGTTATACATGTCTATCAAACCCAGACTTGTCTTCANATGTGAGACTTGCTTTTCAAG	710
Dd		601	CACAGTTATACATGTCTATCAAACCCAGACTTGTCTTCANATGTGAGACTTGCTTTTCAAG	660
Oy		711	AACATATGGATGAAGTAAAGTATGTCCTGAAAGATTTTGGGGGAAAGTTTTCTTACAGAGCT	770
Dd		661	AACATATGGATGAAGTAAAGTATGTCCTGAAAGATTTTGGGGGAAAGTTTTCTTACAGAGCT	720
Oy		771	AAGTATATTTTAG	830
Dd		721	AAGTATATTTTAG	780
Oy		831	TGTGTGTGTATATGCTGTGTGTATGACACACACGATACACACATATATATGAGACATTA	890
Dd		781	TGTGTGTGTATATGCTGTGTGTATGACACACACGATACACACATATATATGAGACATTA	840
Oy		891	AGCCATTTCTAAGACTGTATATGTTATGGAAGSTCTGACTAGSCATGATTTACAGAAAGCA	950
Dd		841	AGCCATTTCTAAGACTGTATATGTTATGGAAGSTCTGACTAGSCATGATTTACAGAAAGCA	900
Oy		951	AGATTGGCATATCAATTTGTATCTAATAAAAAAGCTGACATTGACCCAGACATATTTGTACTCTT	1010
Dd		901	AGATTGGCATATCAATTTGTATCTAATAAAAAAGCTGACATTGACCCAGACATATTTGTACTCTT	960
Oy		1011	CTAAAAATAG	1070
Dd		961	CTAAAAATAG	1020
Oy		1071	CTAAGTAGAGACTTTGAGAGAAATTTCAACAGTGTGTCTTACAGAGTGTTCAGAGCAAGC	1130
Dd		1021	CTAAGTAGAGACTTTGAGAGAAATTTCAACAGTGTGTCTTACAGAGTGTTCAGAGCAAGC	1080
Oy		1131	AAGAAATTGAAGTTGCTCTAGACACAGAGACATTAAGTATCATGTCTCTTTTAATACAGATA	1190
Dd		1081	AAGAAATTGAAGTTGCTCTAGACACAGAGACATTAAGTATCATGTCTCTTTTAATACAGATA	1140

Accession	Sequence	Length
QY	CCCCGAATGAGAAAGGGTGCAGAGGCTCAAAAGGCATTAAGCATTTCCAAATGACCACT	1250
Db	1141 CCCCCAATGAGAAAGGGTGCAGAGGCTCAAAAGGCATTAAGCATTTCCAAATGACCACT	1200
QY	1251 AAGTGTCTCTTTCGGTTTCGTGTCACATGAAACATTTGATTATAGTTAAATCTCTC	1310
Db	1201 AAGTGTCTCTTTCGGTTTCGTGTCACATGAAACATTTGATTATAGTTAAATCTCTC	1260
QY	1311 TATCTTGATCTT	1323
Db	1261 TATCTTGATCTT	1273

RESULT 5

```

US-11-129-861-77
/ Sequence 77, Application US/11129861
/ Publication No. US20060031956A1
/ GENERAL INFORMATION:
/ APPLICANT: Kurachi, Kotoku
/ APPLICANT: Kurachi, Sumiko
/ TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
/ TITLE OF INVENTION: Use Thereof
/ FILE REFERENCE: UM-03603
/ CURRENT APPLICATION NUMBER: US/11/129,861
/ CURRENT FILING DATE: 2005-05-16
/ PRIOR APPLICATION NUMBER: US/09/328,925
/ PRIOR FILING DATE: 1999-06-09
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 77
/ LENGTH: 1273
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-129-861-77

```

Query Match	Score	DB	Length
74.5%	1271.4	11	1273

QY	51	GGGCGCTGACGTAACTAATACATCCCATCTTTGGTAGATTGAAATATATACATCTAT	110
Db	1	GGCCTCTACATACATATACATCTTCCCATCTTTGGTAGATTGAAATATATACATCTAT	60
QY	111	GATCATTTGCTTTTCTCTTTACAGGGGAGATTTCAATTTTACCTGAGCAATTGATTA	170
Db	61	GATCATTTGCTTTTCTCTTTACAGGGGAGATTTCAATTTTACCTGAGCAATTGATTA	120
QY	171	GAATAATGAAACACTAGAGGAATATATATGTTTAGAATAATACAGTCATTTCTAAAGGCC	230
Db	121	GAATAATGAAACACTAGAGGAATATATATGTTTAGAATAATACAGTCATTTCTAAAGGCC	180
QY	231	CAGCCCTTACAAAAATTTGGAAGTTAAATTTCTCCATCTGTCCATCAGATACTATGGTTC	290
Db	181	CAGCCCTTACAAAAATTTGGAAGTTAAATTTCTCCATCTGTCCATCAGATACTATGGTTC	240
QY	291	TCACATATGGCAACTAATCTCATCTCAATTTTCCCTCTTAGACAGCATTCATCTTCCGAT	350
Db	241	TCACATATGGCAACTAATCTCATCTCAATTTTCCCTCTTAGACAGCATTCATCTTCCGAT	300
QY	351	CTTCTTTGCTTCTCCCAACCAAAACATCAATGGTTTATTAAGTTCGTATACAGTACAGATC	410
Db	301	CTTCTTTGCTTCTCCCAACCAAAACATCAATGGTTTATTAAGTTCGTATACAGTACAGATC	360
QY	411	TTTGGTCTACTCTATCAACAAGGCAGATACACACTCATGAAGAAAGACAAGAGTAGC	470
Db	361	TTTGGTCTACTCTATCAACAAGGCAGATACACACTCATGAAGAAAGACAAGAGTAGC	420
QY	471	TGAGAGGCTTAAACTCATCAAAAACGTACTCTTTTTCCTCTACCCATTCCTCAATCTT	530
Db	421	TGAGAGGCTTAAACTCATCAAAAACGTACTCTTTTTCCTCTACCCATTCCTCAATCTT	480

QY	531	TACCTTTGCAAAATCCCAATCCCAATCAGTTTTCTCTTTACTCCCTCTCC	530
Db	481	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTCTCTTTACTCCCTCTCC	540
QY	591	TTTTACCTCCCATGTCGTTAAAGAGAGATGGGAGCATCTTCTGTATACTCTGTGA	650
Db	541	TTTTACCTCCCATGTCGTTAAAGAGAGATGGGAGCATCATCTGTGTATACTCTGTGA	600
QY	651	CACAGTTATACATGTCTATCAAACCCGACCTTGGCTTCATATGTGAGACTGTCTTACG	710
Db	601	CACAGTTATACATGTCTATCAAACCCGACACTGTCTTCATATGTGAGACTGTCTTACG	660
QY	711	AACATPAGGAGTGAAGTAAAGTGCTGACAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATT	770
Db	661	AACATPAGGAGTGAAGTAAAGTGCTGACAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGATT	720
QY	771	AAGTTATTTAG	830
Db	721	AAGTTATTTAG	780
QY	831	TGCTGTGTGTATATGCGTGTGTGTAGACACACAGCATATACACATATATATGAAAGCATAT	890
Db	781	TGCTGTGTGTATATGCGTGTGTGTAGACACACAGCATATACACATATATATGAAAGCATAT	840
QY	891	AGCCATCTAAGACCTTGATGTATATGAGAGTCTGACTAGGCATGATTTTACGAGAGGCA	950
Db	841	AGCCATCTAAGACCTTGATGTATATGAGAGTCTGACTAGGCATGATTTTACGAGAGGCA	900
QY	951	AGATTGGCATATCATTTGTAATCTAAAAAAGCTGACATTTGACCCGACATATTTGTACTCTTT	1010
Db	901	AGATTGGCATATCATTTGTAATCTAAAAAAGCTGACATTTGACCCGACATATTTGTACTCTTT	960
QY	1011	CTAAAAATTAATATATATATATATCTAAACGAAAGAGAGAACCGTTCGTTTGCAATCTACAG	1070
Db	961	CTAAAAATTAATATATATATATATCTAAACGAAAGAGAGAACCGTTCGTTTGCAATCTACAG	1020
QY	1071	CTAGTAGAGACTTTGAGGAGAAATTCACACGTGTCTTCACGACGTTCAGAGCCACAGC	1130
Db	1021	CTAGTAGAGACTTTGAGGAGAAATTCACACGTGTCTTCACGACGTTCAGAGCCACAGC	1080
QY	1131	AAGAGATTGAAGTTGCCCTPAGACGAGAGGACATAGTATCATGTCTCCCTTAACTACAGATA	1190
Db	1081	AAGAGATTGAAGTTGCCCTPAGACGAGAGGACATAGTATCATGTCTCCCTTAACTACAGATA	1140
QY	1191	CCCCGAGTGAAGAGAGGGTGCAGCAGGCTCAAAAGGCATAAAGCTCATTCGATCAGCCCACT	1250
Db	1141	CCCCGAGTGAAGAGAGGGTGCAGCAGGCTCAAAAGGCATAAAGCTCATTCGATCAGCCCACT	1200
QY	1251	AAGTTGTCCTTTTCGTTTCTGTGTTCACCATGGAACATTTTGATATAGTATATCCCTTC	1310
Db	1201	AAGTTGTCCTTTTCGTTTCTGTGTTCACCATGGAACATTTTGATATAGTATATCCCTTC	1260
QY	1311	TATCTGTAATCTT 1323	
Db	1261	TATCTGTAATCTT 1273	

RESULT 6

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US-11-129-861-78
; Sequence 78, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/11/129,861
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/328,925
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0

```

SEQ ID NO 78
 LENGTH: 1273
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-11-129-861-78

Query Match 74.4%; Score 1269.8; DB 11; Length 1273;
 Best Local Similarity 99.8%; Pred. No. 2.7e-61; Indels 0; Gaps 0;
 Matches 1271; Conservative 0; Mismatches 2;

51 GGCCTCTCACTAATCAATCACTTCCATCTTTGTTAGATTGATATATACATTTAT 110
 1 GGCCTCTCACTAATCAATCACTTCCATCTTTGTTAGATTGATATATACATTTAT 60
 111 GATCATTTGCTTTTCTTTTACAGGGGAGATTTCATATTTCCTGAGCAATTGATTA 170
 61 GATCATTTGCTTTTCTTTTACAGGGGAGATTTCATATTTCCTGAGCAATTGATTA 120
 171 GAAATGGAACCACTAGAGAAATATATGTTAGAAATTACAGTCAATTTCTAAGGGCC 230
 121 GAAATGGAACCACTAGAGAAATATATGTTAGAAATTACAGTCAATTTCTAAGGGCC 180
 231 CAGCCCTTGACAAATTTGAGATTAAATTCCTCATCTGTCATCATATCATATGTTTC 290
 181 CAGCCCTTGACAAATTTGAGATTAAATTCCTCATCTGTCATCATATCATATGTTTC 240
 291 TCCACTATGGAACCACTATCACTCAATTTCCCTCTTACAGCATTCATTTCCCAT 350
 241 TCCACTATGGAACCACTATCACTCAATTTCCCTCTTACAGCATTCATTTCCCAT 300
 351 CTCTTTGCTCTTCCAAACCAATCAATGTTTATAGTTCTGATACAGTACAGATTC 410
 301 CTCTTTGCTCTTCCAAACCAATCAATGTTTATAGTTCTGATACAGTACAGATTC 360
 411 TTTGCTACTATCTATCAAGGCCAGTACCACTCATATGAGAAAGAACAGAGATGAC 470
 361 TTTGCTACTATCTATCAAGGCCAGTACCACTCATATGAGAAAGAACAGAGATGAC 420
 471 TGAGAGGCTTAAACATCAATCAAAACATACCTCTTCTGACCTTATCTGCAATCTT 530
 421 TGAGAGGCTTAAACATCAATCAAAACATACCTCTTCTGACCTTATCTGCAATCTT 480
 531 TTACCTTTTCCAAATCCCAATCCCAATAGTTTCTCTTCTTACTCCCTCTCC 590
 481 TTACCTTTTCCAAATCCCAATCCCAATAGTTTCTCTTCTTACTCCCTCTCC 540
 591 TTTTACCCTCCATGCTGTTTAAAGAGATGGGAGCATCTGTTTATATCTTCTGTA 650
 541 TTTTACCCTCCATGCTGTTTAAAGAGATGGGAGCATCTGTTTATATCTTCTGTA 600
 651 CACACTTATACATGCTATCAAAACCACTGCTTCCATATGAGACTTCTTTTCCAG 710
 601 CACACTTATACATGCTATCAAAACCACTGCTTCCATATGAGACTTCTTTTCCAG 660
 711 AACATAGGAGATGAGTATAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTCCAGAGATT 770
 661 AACATAGGAGATGAGTATAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTCCAGAGATT 720
 771 AAGTATTTTAG 830
 721 AAGTATTTTAG 780
 831 TGTGTGTGTATATGCTGTGTGTATACACACGATATACACATATATATATATATATAG 890
 781 TGTGTGTGTATATGCTGTGTGTATACACACGATATACACATATATATATATATATAG 840
 891 AGCCATTTCAAGAGCTTGTATATGTTATGAGAGTCTGATAGAGATTTTCCAGAGGCA 950
 841 AGCCATTTCAAGAGCTTGTATATGTTATGAGAGTCTGATAGAGATTTTCCAGAGGCA 900
 951 AGATTGGCATATCATTTGATCAAAAAAGCTGACATTGACCAAGCATATTTGACTCTTT 1010

901 AGATTGGCATATCATTTGATCAAAAAAGCTGACATTGACCAAGCATATTTGACTCTTT 960
 1011 CTAAAAATATATATATATATGCTATACAGAAAGAACCGTTGTTGCAATCTACAG 1070
 961 CTAAAAATATATATATATATATGCTATACAGAAAGAACCGTTGTTGCAATCTACAG 1020
 1071 CTATAGAGACTTTTGAAGAGAAATTCACAGTGTCTTTCAGCAGTGTTCAGAGCCAGC 1130
 1021 CTATAGAGACTTTTGAAGAGAAATTCACAGTGTCTTTCAGCAGTGTTCAGAGCCAGC 1080
 1131 AAGAGTTGAAGTCTTACAGCAGAGACATATATATATATATATATATATATATATAG 1190
 1081 AAGAGTTGAAGTCTTACAGCAGAGACATATATATATATATATATATATATATATAG 1140
 1191 CCCCAGATGGAAGAGGGGTCAGAGGCTCAAGGCAATATAGTCAATTCAGGCAACT 1250
 1141 CCCCAGATGGAAGAGGGGTCAGAGGCTCAAGGCAATATAGTCAATTCAGGCAACT 1200
 1251 AAGTGTCTTCTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 1310
 1201 AAGTGTCTTCTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 1260
 1311 TATCTTGAATCTT 1323
 1261 TATCTTGAATCTT 1273

RESULT 7
 US-11-129-861-79
 ; Sequence 79, Application US/11129861
 ; Publication No. US20060031956A1

GENERAL INFORMATION:
 APPLICANT: Kurachi, Sumiko
 TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
 FILE REFERENCE: UM-03603
 CURRENT APPLICATION NUMBER: US/11/129, 861
 CURRENT FILING DATE: 2005-05-16
 PRIOR APPLICATION NUMBER: US/09/328, 925
 PRIOR FILING DATE: 1999-06-09
 NUMBER OF SEQ ID NOS: 84
 SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 79
 ; LENGTH: 1273
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-11-129-861-79

Query Match 74.2%; Score 1266.6; DB 11; Length 1273;
 Best Local Similarity 99.7%; Pred. No. 4e-61; Indels 4; Gaps 0;
 Matches 1269; Conservative 0; Mismatches 4;

51 GGCCTCTCACTAATCAATCACTTCCATCTTTGTTAGATTGATATATACATTTAT 110
 1 GGCCTCTCACTAATCAATCACTTCCATCTTTGTTAGATTGATATATACATTTAT 60
 111 GATCATTTGCTTTTCTTTTACAGGGGAGATTTCATATTTCCTGAGCAATTGATTA 170
 61 GATCATTTGCTTTTCTTTTACAGGGGAGATTTCATATTTCCTGAGCAATTGATTA 120
 171 GAAATGGAACCACTAGAGAAATATATGTTAGAAATTACAGTCAATTTCTAAGGGCC 230
 121 GAAATGGAACCACTAGAGAAATATATGTTAGAAATTACAGTCAATTTCTAAGGGCC 180
 231 CAGCCCTTGACAAATTTGAGATTAAATTCCTCATCTGTCATCATATCATATGTTTC 290
 181 CAGCCCTTGACAAATTTGAGATTAAATTCCTCATCTGTCATCATATCATATGTTTC 240
 291 TCCACTATGGAACCACTATCACTCAATTTCCCTCTTACAGCATTCATTTCCCAT 350

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Db 241 TCACATAGGCACTACCTCACTGATTTTCCCTCTTGAAGCATTCCATCTTCCGAT 300
Qy 351 CTTCTTTGCTTCCACCAAAACATCAATGTTTATTAAGTCTGTATACAGTACAGATC 410
Db 301 CTTCTTTGCTTCCACCAAAACATCAATGTTTATTAAGTCTGTATACAGTACAGATC 360
Qy 411 TTTGGTCTACTATACAAAGGCGATACACATCTATAGAAAGAAACACAGAGTAC 470
Db 361 TTTGGTCTACTATACAAAGGCGATACACATCTATAGAAAGAAACACAGAGTAC 420
Qy 471 TGAGAGGCTAAATCATCAAAAACATCTCTCTTTCCCTCAACCTTATCTCTCATCTT 530
Db 421 TGAGAGGCTAAATCATCAAAAACATCTCTCTTTCCCTCAACCTTATCTCTCATCTT 480
Qy 531 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 590
Db 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
Qy 591 TTTTACCCCTCCAGTGGCTTAAAGAGAGATGGGAGCATCTCTGTATACCTCTGTAT 650
Db 541 TTTTACCCCTCCAGTGGCTTAAAGAGAGATGGGAGCATCTCTGTATACCTCTGTAT 600
Qy 651 CACAGTTATACATGCTATCAAAACCAAGCTTCTCTCAATGAGAGACTTCTCTTCAAG 710
Db 601 CACAGTTATACATGCTATCAAAACCAAGCTTCTCTCAATGAGAGACTTCTCTTCAAG 660
Qy 711 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAAGAGTT 770
Db 661 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAAGAGTT 720
Qy 771 AAGTTATTTATATATATATATATATATATATATATATATATATATATATATATAT 830
Db 721 AAGTTATTTATATATATATATATATATATATATATATATATATATATATATATAT 780
Qy 831 TGTGTGTGTATGCGTGTGTGTAGACACACGACATACACATATATATATATATATAT 890
Db 781 TGTGTGTGTATGCGTGTGTGTAGACACACGACATACACATATATATATATATATAT 840
Qy 891 AGCCATTTCAAGAGCTTGTATGTTTATGAGAGTCTGATAGGATATATTCACAGAGGA 950
Db 841 AGCCATTTCAAGAGCTTGTATGTTTATGAGAGTCTGATAGGATATATTCACAGAGGA 900
Qy 951 AAGTTGGCATATCTTGAATCTTAACTAAAGAGCTGACATTCACCAATATTTGACTCTT 1010
Db 901 AAGTTGGCATATCTTGAATCTTAAAGAGCTGACATTCACCAATATTTGACTCTT 960
Qy 1011 CTTAAATATATATATATATATATATATATATATATATATATATATATATATATAT 1070
Db 961 CTTAAATATATATATATATATATATATATATATATATATATATATATATATATAT 1020
Qy 1071 CTAAGTACAGATCTTTGAGAAAGATTAACAAGTGTCTTCAAGAGTTCACAGCCAGC 1130
Db 1021 CTAAGTACAGATCTTTGAGAAAGATTAACAAGTGTCTTCAAGAGTTCACAGCCAGC 1080
Qy 1131 AAGAGTTAAGTGTCTGACAGAGAGATTAAGTATGATCTCTCTTTAATCTAGCATA 1190
Db 1081 AAGAGTTAAGTGTCTGACAGAGAGATTAAGTATGATCTCTCTTTAATCTAGCATA 1140
Qy 1191 CCCCGAAGTGAAGAGGAGTGCAGAGAGCTCAAGGATTAAGTCAATCAGCCAGCT 1250
Db 1141 CCCCGAAGTGAAGAGGAGTGCAGAGAGCTCAAGGATTAAGTCAATCAGCCAGCT 1200
Qy 1251 AAGTGTCTCTTTCTGTTTCTGTTTCAACATAGAAATTTGATTAAGTATCTTTC 1310
Db 1201 AAGTGTCTCTTTCTGTTTCTGTTTCAACATAGAAATTTGATTAAGTATCTTTC 1260
Qy 1311 TATCTGAATCTT 1323
Db 1261 TATCTGAATCTT 1273
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RESULT 8

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US-11-129-861-82
; Sequence 82, Application US/11129861
; Publication No. US20060031956A1
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/328,925
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 82
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-129-861-82
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Query Match 73.9%; Score 1261; DB 11; Length 1272;
Best Local Similarity 99.9%; Pred. No. 86-61;
Matches 1272; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy 51 GGCCTCTACATCACTCACTTCCCAATCTTTGATTAAGTGAATATACATTTCTAT 110
Db 1 GGCCTCTACATCACTCACTTCCCAATCTTTGATTAAGTGAATATACATTTCTAT 60
Qy 111 GATCATGCTTTTCTCTTACAGAGGAGATTCATATTTTACCTGAGCAATGATTA 170
Db 61 GATCATGCTTTTCTCTTACAGAGGAGATTCATATTTTACCTGAGCAATGATTA 120
Qy 171 GAAATGGAACCACTAGAGGAATATATATGTTAGAAATTAACATCTTTCAAGGCGC 230
Db 121 GAAATGGAACCACTAGAGGAATATATATGTTAGAAATTAACATCTTTCAAGGCGC 180
Qy 231 CAGCCCTTGACAAATGGAAGTTAAATTCCTCACTCTGTCATCAGATCATAGTTC 290
Db 181 CAGCCCTTGACAAATGGAAGTTAAATTCCTCACTCTGTCATCAGATCATAGTTC 240
Qy 291 TCACATAGGCACTCACTCAATTTTCCCTCTTACAGAGATTCATCTTCCGAT 350
Db 241 TCACATAGGCACTCACTCAATTTTCCCTCTTACAGAGATTCATCTTCCGAT 300
Qy 351 CTTCTTTGCTTCCACCAAAACATCAATGTTTATTAAGTCTGTATACAGTACAGATC 410
Db 301 CTTCTTTGCTTCCACCAAAACATCAATGTTTATTAAGTCTGTATACAGTACAGATC 360
Qy 411 TTTGGTCTACTATACAAAGGCGATACACATCTATAGAAAGAAACACAGAGTAC 470
Db 361 TTTGGTCTACTATACAAAGGCGATACACATCTATAGAAAGAAACACAGAGTAC 420
Qy 471 TGAGAGGCTAAATCATCAAAAACATCTCTCTTTCCCTCAACCTTATCTCTCATCTT 530
Db 421 TGAGAGGCTAAATCATCAAAAACATCTCTCTTTCCCTCAACCTTATCTCTCATCTT 480
Qy 531 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 590
Db 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
Qy 591 TTTTACCCCTCCAGTGGCTTAAAGAGAGATGGGAGCATCTCTGTATACCTCTGTAT 650
Db 541 TTTTACCCCTCCAGTGGCTTAAAGAGAGATGGGAGCATCTCTGTATACCTCTGTAT 600
Qy 651 CACAGTTATACATGCTATCAAAACCAAGCTTCTCTCAATGAGAGACTTCTCTTCAAG 710
Db 601 CACAGTTATACATGCTATCAAAACCAAGCTTCTCTCAATGAGAGACTTCTCTTCAAG 660
Qy 711 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAAGAGTT 770
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FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3654
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
US-11-128-061-3654

Query Match 60.2%; Score 1027; DB 14; Length 1400;
Best Local Similarity 100.0%; Pred. No. 2,8e-48;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAAAGATGATTTCCAGGTTAATTCATTGGAAATTAACAGGGCCCTCTCAC 60
DB 361 AATGAAAGATGATTTCCAGGTTAATTCATTGGAAATTAACAGGGCCCTCTCAC 420
QY 61 TAACATACCTTCCATCTTTGTTAGATTGAATATATACATTCATATGATTCCT 120
DB 421 TAACATACCTTCCATCTTTGTTAGATTGAATATATACATTCATATGATTCCT 480
QY 121 TTTTCTCTTACAGGGAGAAATTTTCATATTTTACCTGAGCAATGATTAGAAATGGA 180
DB 481 TTTTCTCTTACAGGGAGAAATTTTCATATTTTACCTGAGCAATGATTAGAAATGGA 540
QY 181 CCATGAGGAATATATATGTGTAGAGAAATTCAGTCAATTTCTAAGGGCCAGCCCTTGA 240
DB 541 CCATGAGGAATATATATGTGTAGAGAAATTCAGTCAATTTCTAAGGGCCAGCCCTTGA 600
QY 241 CAAATTTGTAAGTTAATTTCCATCTGTCATCAGATCTATGTTTCCACTATAG 300
DB 601 CAAATTTGTAAGTTAATTTCCATCTGTCATCAGATCTATGTTTCCACTATAG 660
QY 301 CAACCTACTCACTCAATTTTCCCTCTTACGAGCATTCCTCCGATCTTCTTGGCT 360
DB 661 CAACCTACTCACTCAATTTTCCCTCTTACGAGCATTCCTCCGATCTTCTTGGCT 720
QY 361 TCTCCACCAAAACATCAATTTTATATAGTTCTGTATACATACAGATCTTGGCTCAC 420
DB 721 TCTCCACCAAAACATCAATTTTATATAGTTCTGTATACATACAGATCTTGGCTCAC 780
QY 421 TCTATCAAGGCGCATACACATCTGATGAGAAAGAACAGAGATGAGAGGCTA 480
DB 781 TCTATCAAGGCGCATACACATCTGATGAGAAAGAACAGAGATGAGAGGCTA 840
QY 481 AACTCATCAAAACACTACTCTTTTCTCTACCTTATTCCTCAATCTTTTACCTTTTC 540
DB 841 AACTCATCAAAACACTACTCTTTTCTCTACCTTATTCCTCAATCTTTTACCTTTTC 900
QY 541 CAAATCCCAATCCCAATCAATTTTCTCTTCTTACCTCTCTCCCTTTTACCTCTC 600
DB 901 CAAATCCCAATCCCAATCAATTTTCTCTTCTTACCTCTCTCCCTTTTACCTCTC 960
QY 601 CATGCTGTAAAGAGAGATGAGGAGCATCATCTGTATATCTTCTGTACAGATTATA 660
DB 961 CATGCTGTAAAGAGAGATGAGGAGCATCATCTGTATATCTTCTGTACAGATTATA 1020
QY 661 CATGCTGTAAAGAGATGAGGAGCATCATCTGTATATCTTCTGTACAGATTATA 720
DB 1021 CATGCTGTAAAGAGATGAGGAGCATCATCTGTATATCTTCTGTACAGATTATA 1080
QY 721 TGAAGTAAAGGCTGTAAGTTTGGGGGAAAGTTTCTTCAAGAGTTAAAGTTATTT 780
DB 1081 TGAAGTAAAGGCTGTAAGTTTGGGGGAAAGTTTCTTCAAGAGTTAAAGTTATTT 1140
QY 781 AT 840
DB 1141 AT 1200

QY 841 TATGCTGTGTATAGACACACAGCATACACATATATATATATATATATATATATATATAT 900
DB 1201 TATGCTGTGTATAGACACACAGCATACACATATATATATATATATATATATATATATAT 1260
QY 901 AGAGCTGTATGCTTATGAGAGTCTGATAGCATATTTTACGAAAGCATATTTGGCAT 960
DB 1261 AGAGCTGTATGCTTATGAGAGTCTGATAGCATATTTTACGAAAGCATATTTGGCAT 1320
QY 961 ATCATTTATCAATTAAGTATGAGCATGAGCCAGACATATTTTCTTTTAAATATA 1020
DB 1321 ATCATTTATCAATTAAGTATGAGCATGAGCCAGACATATTTTCTTTTAAATATA 1380
QY 1021 TAATAT 1027
DB 1381 TAATAT 1387

RESULT 12
US-11-128-049-3654
Sequence 3654, Application US/11/128049
Publication No. US2006010513A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane B.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
PRIOR FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3654
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
US-11-128-049-3654

Query Match 60.2%; Score 1027; DB 14; Length 1400;
Best Local Similarity 100.0%; Pred. No. 2,8e-48;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TAACATACCTTCCATCTTTGTTAGATTGAATATATACATTCATATGATTCCT 120
DB 421 TAACATACCTTCCATCTTTGTTAGATTGAATATATACATTCATATGATTCCT 480
QY 121 TTTTCTCTTACAGGGAGAAATTTTCATATTTTACCTGAGCAATGATTAGAAATGGA 180
DB 481 TTTTCTCTTACAGGGAGAAATTTTCATATTTTACCTGAGCAATGATTAGAAATGGA 540
QY 181 CCATGAGGAATATATATGTGTAGAGAAATTCAGTCAATTTCTAAGGGCCAGCCCTTGA 240
DB 541 CCATGAGGAATATATATGTGTAGAGAAATTCAGTCAATTTCTAAGGGCCAGCCCTTGA 600
QY 241 CAAATTTGTAAGTTAATTTCTCCATCTGTCATCAGATCTATGTTTCCACTATAG 300
DB 601 CAAATTTGTAAGTTAATTTCTCCATCTGTCATCAGATCTATGTTTCCACTATAG 660
QY 301 CAACCTACTCACTCAATTTTCCCTCTTACGAGCATTCCTCCGATCTTCTTGGCT 360
DB 661 CAACCTACTCACTCAATTTTCCCTCTTACGAGCATTCCTCCGATCTTCTTGGCT 720

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QY 361 TCTCCAAACCAAAACATCAATGTTTATTAGTCTGTATAGACAGATCTTGTGCTAC 420
DB 721 TCTCCAAACCAAAACATCAATGTTTATTAGTCTGTATAGACAGATCTTGTGCTAC 780
QY 421 TCTATCAAGGCGCAGTACCACTCATGAGAGAAACACAGAGTAGTGAAGGCTA 480
DB 781 TCTATCAAGGCGCAGTACCACTCATGAGAGAAACACAGAGTAGTGAAGGCTA 840
QY 481 AAATCATCAAAAACATCACTCTCTTTCTCTACCTTATCTCTCATCTTTTCTTTT 540
DB 841 AAATCATCAAAAACATCACTCTCTTTCTCTACCTTATCTCTCATCTTTTCTTTT 900
QY 541 CAAATCCCAATCCCAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
DB 901 CAAATCCCAATCCCAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
QY 601 CATGCTGTAAAGAGAGATGGGAGACATCTCTGTATATCTTGTATACAGAGTTA 660
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DB 1141 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1200
QY 841 TATGCTGTGTGAGACACACAGCATACACATATATATGAGAGATAGCATTTCTA 900
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QY 901 AAGCTGTATGTTATGAGAGTCTGACATGAGCATATTTTCAAGAGGCAAGATGGCAT 960
DB 1261 AAGCTGTATGTTATGAGAGTCTGACATGAGCATATTTTCAAGAGGCAAGATGGCAT 1320
QY 961 ATCATTTGTAATAAAAAGCTGACATTTGACCCAGACATATTTTCTTAAAAATTA 1020
DB 1321 ATCATTTGTAATAAAAAGCTGACATTTGACCCAGACATATTTTCTTAAAAATTA 1380
QY 1021 TATATAT 1027
DB 1381 TATATAT 1387

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TYPE: DNA
ORGANISM: Homo sapiens
US-11-128-061-12
Query Match 60.2%; Score 1027; DB 14; Length 2458;
Best Local Similarity 100.0%; Pred. No. 2,1e-48;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TAACTAATCACTTCCCATCTTTTGTAGATTGAATATATATATATATATATATATAT 120
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QY 121 TTTTCTTTTACAGGGGAGAAATTTTCAATATTTTACCGAGACAAATGATTAAGAAATGAA 180
DB 1539 TTTTCTTTTACAGGGGAGAAATTTTCAATATTTTACCGAGACAAATGATTAAGAAATGAA 1598
QY 181 CCACTAGAGAAATATATATGTTATAGAAATTAAGATCATTTCTAAGGGCCAGCCCTTGA 240
DB 1599 CCACTAGAGAAATATATATGTTATAGAAATTAAGATCATTTCTAAGGGCCAGCCCTTGA 1658
QY 241 CAAATTTGTAAGTTAAATTTCTCACTGTCTCCATCAATATATATATATATATATAT 300
DB 1659 CAAATTTGTAAGTTAAATTTCTCACTGTCTCCATCAATATATATATATATATATAT 1718
QY 301 CAATTAATCACTCAATTTTCCCTCTTGTAGAGCATTCATCTCCGATCTTCTTGTCT 360
DB 1719 CAATTAATCACTCAATTTTCCCTCTTGTAGAGCATTCATCTCCGATCTTCTTGTCT 1778
QY 361 TCTCCAAACCAAAACATCAATGTTTATTAGTCTGTATAGACAGATCTTGTGCTAC 420
DB 1779 TCTCCAAACCAAAACATCAATGTTTATTAGTCTGTATAGACAGATCTTGTGCTAC 1838
QY 421 TCTATCAAGGCGCAGTACCACTCATGAGAGAAACACAGAGTAGTGAAGGCTA 480
DB 1839 TCTATCAAGGCGCAGTACCACTCATGAGAGAAACACAGAGTAGTGAAGGCTA 1898
QY 481 AAATCATCAAAAACATCACTCTCTTTCTCTACCTTATCTCTCATCTTTTCACTTTT 540
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DB 1959 CAAATCCCAATCCCAATCAATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2018
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DB 2019 CATGCTGTAAAGAGAGATGGGAGACATCTCTGTATATCTTGTATACAGATTTA 2078
QY 661 CATGCTGTAAACCAAGACTGCTTCATATGAGAGACTTCTTTTCAAGACATAGGA 720
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QY 781 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 840
DB 2199 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2258
QY 841 TATGCTGTGTGAGACACACAGCATACACATATATATGAGAGATAGCATTTCTA 900
DB 2259 TATGCTGTGTGAGACACACAGCATACACATATATATGAGAGATAGCATTTCTA 2318
QY 901 AAGCTGTATGTTATGAGAGTCTGACATGAGCATATTTTCAAGAGGCAAGATGGCAT 960
DB 2319 AAGCTGTATGTTATGAGAGTCTGACATGAGCATATTTTCAAGAGGCAAGATGGCAT 2378
QY 961 ATCATTTGTAATAAAAAGCTGACATTTGACCCAGACATATTTTCTTAAAAATTA 1020

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Db	2379	ATCATTGTAACCTTAAAAAGCTGACATGACCCAGACATATTGTACTCTTTCTAAAAATTA	2438
Qy	1021	TAATTAAT	1027
Db	2439	TAATTAAT	2445

RESULT 14
US-11-128-049-12

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Sequence 12 Application US/11128049
Publication No. US20060010513A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane B.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OR INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
TITLE OR INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128, 049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 2458
TYPE: DNA
ORGANISM: Homo sapiens
IS-11-128-049-12

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Query Match	60.2%;	Score 1027;	DB 14;	Length 2458;
Best Local Similarity	100.0%;	Pred. No. 2.1e-48;		
Matches 1027; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	ATATGAAGATGGAATTTCCAGGTTAAATTCATATGGAATGGAAATTAACAGGGCCCTCAC	60
Db	1419	AATGAAAGATGGAATTTCCAGGTTAAATTCATATGGAATGGAAATTAACAGGGCCCTCAC	1478
QY	61	TAACTAAATGACTTTCCACTCTTTGTTAGATTGAAATATATATACATTCATGATCATTTGCT	120
Db	1479	TAACTAAATGACTTTCCACTCTTTGTTAGATTGAAATATATATACATTCATGATCATTTGCT	1538
QY	121	TTTTCCTCTTAACAGGGAGAAATTCATATTTTACCTAGAGAAATGATTTTGAAAAATGAA	180
Db	1539	TTTTCCTCTTAACAGGGAGAAATTCATATTTTACCTAGAGAAATGATTTTGAAAAATGAA	1598
QY	181	CCACTAGAGAAATTAATGTGTTAGAAATTAACAGTATTTCTAAGGGCCAGCCCTTGA	240
Db	1599	CCACTAGAGAAATTAATGTGTTAGAAATTAACAGTATTTCTAAGGGCCAGCCCTTGA	1658
QY	241	CAAAATGTGGAAGTTAAATTCCTCACTGTGCCATCGAATCTATGTTCTTCCACTATGG	300
Db	1659	CAAAATGTGGAAGTTAAATTCCTCACTGTGCCATCGAATCTATGTTCTTCCACTATGG	1718
QY	301	CAACTAATCACTCAATTTTCCCTCCTTAGACAGATTCACATCTCCGATCTTCTTGGT	360
Db	1719	CAACTAATCACTCAATTTTCCCTCCTTAGACAGATTCACATCTTCCGATCTTCTTGGT	1778
QY	361	TCTTCAACCAAAACATCAATGTTTATTTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC	420
Db	1779	TCTTCAACCAAAACATCAATGTTTATTTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC	1838
QY	421	TCTATCAACAAGGCCAGTACACACTCATGTGAAGAAAGAACACAGAGATGCTGAGAGCTTA	480
Db	1839	TCTATCAACAAGGCCAGTACACACTCATGTGAAGAAAGAACACAGAGATGCTGAGAGCTTA	1898
QY	481	AAACTCATCAAAAACACTACTCTTCTTCTCTTACCCATTCCTCAATCTTTTACCTTTTC	540

[illegible]

RESULT 15
US-09-925

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? Sequence 808251, Application US/09925065A
? Publication No. US20040181048A1
? GENERAL INFORMATION:
? APPLICANT: Wang, David G.
? TITLE OF INVENTION: Identification and Mapping of Single
? TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
? FILE REFERENCE: 108827.135
? CURRENT APPLICATION NUMBER: US/09/925,065A
? PRIOR FILING DATE: 2001-08-08
? PRIOR APPLICATION NUMBER: US 60/243, 096
? PRIOR FILING DATE: 2000-10-24
? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250, 092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/251,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,946
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 808251
? LENGTH: 581
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-925-065A-808251

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Query Match	13.5%	Score 229.8;	DB 6;	Length 581;
Best Local Similarity	99.1%	Pred. No. 2.8e-05;		
Matches 231; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1473	CTGACCCGCGAAGCTGCTGCTTCTCCGCGCCCAACCTCACCCTCCAGCCAGCTCACT	1532
Db	1	CTGACCCGCGAAGCTGCTGCTTCTCCGCGCCCAACCTCACCCTCCAGCCAGCTCACT	60
Qy	1533	CTTGCTAGTTCCTTATGTTCTTTATGTCATATATTTTGTCTTGCAATATATGATATAA	1592
Db	61	CTTGCTAGTTCCTTATGTTCTTTATGTCATATATTTTGTCTTGCAATATATGATATAA	120
Qy	1593	TAAACATATTTTAAATTTCTTGCTGGGCCCAAGTGGCTCAGGCTATATATCCAGCACT	1652
Db	121	TAAACATATTTTAAATTTCTTGCTGGGCCCAAGTGGCTCAGGCTATATATCCAGCACT	180
Qy	1653	TCTGAGGCCAAGTGGCGGATCACTGAGGTTAGAGTTTCAGGCCAAGCT	1705
Db	181	TCTGAGGCCAAGTGGCGGATCACTGAGGTTAGAGTTTCAGGCCAAGCT	233

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 Job time : 1049.42 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-884-901a-8
Perfect score: 154
Sequence: 1 gttcgtgctgcgcctctctgaa.....ggtcagagacctctctggtgc 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	154	100.0	328	6	AX379350 Sequence
3	154	100.0	771	6	AX379345 Sequence
4	154	100.0	774	8	HSU32510 Human apoli
5	154	100.0	41907	6	AX358722 Sequence
6	154	100.0	41907	8	AF050154 Homo sapi
7	154	100.0	107567	8	AC011481 Homo sapi
8	142	92.2	208239	14	AC021988 Homo sapi
9	141.2	91.7	39483	14	AC146473 Hylobates
10	139.6	90.6	183798	14	AC145523 Papio ham
11	136.4	88.6	231234	14	AC148222 Colobus g
12	131.6	85.5	4097	8	HSU35114 Human apoli
13	131.6	85.5	63931	14	AC120211 Pan trogl
14	130	84.4	183798	14	AC145523 Papio ham
15	114.4	74.3	185724	14	AC146285 Callitru
16	112.8	73.2	191327	14	AC151887 Saimiri b
17	111.4	72.3	186842	14	AC146283 Callitru
18	111.2	72.2	193027	14	AC146520 Aotus nan

C	19	104.2	67.7	183536	14	AC135911 Lemur cat
	20	82	53.2	90	6	AR595858 Sequence
	21	82	53.2	90	6	AR595862 Sequence
	22	78	50.6	82	6	AR595864 Sequence
	23	77	50.0	82	6	AR595860 Sequence
	24	76.4	49.6	221553	9	AC145282
	25	76.4	49.6	226998	14	AC127479
	26	76.4	49.6	237653	14	AC073760
	27	74	48.1	78	6	AR595861 Sequence
	28	74	48.1	78	6	AR595865 Sequence
	29	73.2	47.5	263682	14	AC120709
	30	70	45.5	70	6	AR595863 Sequence
	31	69	44.8	70	6	AR595859 Sequence
	32	37.4	24.3	210122	14	AC108618
	33	37.4	24.3	212946	14	AC110830
	34	37.4	24.3	306529	14	AC109083
	35	35.2	22.9	214674	14	AC164341
	36	35	22.7	135384	4	AC152565
	37	35	22.7	204375	14	AC117045
	38	35	22.7	225735	14	AC106386
	39	34.8	22.6	139711	14	AC153093
	40	34.8	22.6	158972	14	AC160538
	41	34.8	22.6	184010	9	AC113976
	42	34.8	22.6	222681	14	AC137528
	43	34.8	22.6	230167	14	AC097156
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ALIGNMENTS

RESULT 1	AX379349	154 bp	DNA	Linear	PAT 18-MAR-2002
LOCUS	AX379349	Sequence 8 from Patent WO0198482.			
DEFINITION	AX379349				
ACCESSION	AX379349.1	GI:19575189			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1	Miao, C.H. and Kay, M.A.			
AUTHORS					
TITLE	Liver-specific gene expression cassettes, and methods of use				
JOURNAL	Patent: WO 0198482-A 8 27-DEC-2001;				
	The Board of Trustees of The Leland Stanford Junior University (US)				
	; The University of Washington (US)				
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	Best Local Similarity	100.0%; Pred. No. 4,9e-43; Indels 0; Gaps 0;
	Matches	154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	GTTCGTGCTGCTCTGAGTCACTGACAACTTCAAGCTTCAATGCTTCCCTTAA 60
DB	1	GTTTCGTGCTGCTCTGAGTCACTGACAACTTCAAGCTTCAATGCTTCCCTTAA 60
QY	61	ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGCCCTCCCTGCGCTGACCTT 120
DB	61	ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGCCCTCCCTGCGCTGACCTT 120
QY	121	GGAGCTGGGCGAGAGTTCAGAGACTCTCTGGGC 154
DB	121	GGAGCTGGGCGAGAGTTCAGAGACTCTCTGGGC 154

RESULT 2
AX379350 328 bp DNA linear PAT 18-MAR-2002

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX379350
Sequence 9 from Patent WO0198482.
AX379350
AX379350.1 GI:19575190

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Miao, C.H. and Kay, M.A.
Liver-specific gene expression cassettes, and methods of use
Patent: WO 0198482-A 9 27-DEC-2001;
The Board of Trustees of The Ireland Stanford Junior University (US)
; The University of Washington (US)
Location/Qualifiers
1. 328
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

1. 328
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACTTCAGCTACTCATGCTCCCTAAA 60
|
78 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACTTCAGCTACTCATGCTCCCTAAA 137
|
Qy 61 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 120
|
Db 138 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 197
|
Qy 121 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 154
|
Db 198 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 231
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RESULT 3
AX379345 771 bp DNA linear PAT 18-MAR-2002

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX379345
Sequence 4 from Patent WO0198482.
AX379345
AX379345.1 GI:19575185

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Miao, C.H. and Kay, M.A.
Liver-specific gene expression cassettes, and methods of use
Patent: WO 0198482-A 4 27-DEC-2001;
The Board of Trustees of The Ireland Stanford Junior University (US)
; The University of Washington (US)
Location/Qualifiers
1. 771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

1. 771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 771;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACTTCAGCTACTCATGCTCCCTAAA 60
|
Qy 61 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 120
|
Db 141 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 200
|
Qy 121 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 154
|
Db 201 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 234
|

Db 78 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACTTCAGCTACTCATGCTCCCTAAA 137
|
Qy 61 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 120
|
Db 138 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 197
|
Qy 121 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 154
|
Db 198 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 231
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RESULT 4
HSU32510 774 bp DNA linear PRI 31-JAN-1996

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HSU32510
Human apolipoprotein E/C-I gene locus, hepatic control region
HCR-1.
U32510
U32510.1 GI:975886

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

1
Dang, O., Walker, D., Taylor, S., Allan, C., Chin, P., Fan, J. and
Taylor, J.
Structure of the hepatic control region of the human apolipoprotein
E/C-I gene locus
J. Biol. Chem. 270 (38), 22577-22585 (1995)
7673250
2 (bases 1 to 774)
Dang, O., Walker, D., Taylor, S., Allan, C., Chin, P., Fan, J. and
Taylor, J.
Direct Submission
Submitted (26-JUL-1995) John Taylor, Cardiovascular Disease,
GlaxoSmithKline, Institute of Cardiovascular Disease, P.O. Box 419100, San
Francisco, CA 94141-9100, USA
Location/Qualifiers
1. 774
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q"
/tissue_type="placenta"
1. 774
/standard_name="HCR-1"
/note="APOC1 and APOE genes"
/function="hepatic control region"

FEATURES
source

misc_signal

1. 774
/standard_name="HCR-1"
/note="APOC1 and APOE genes"
/function="hepatic control region"

ORIGIN

Query Match 100.0%; Score 154; DB 8; Length 774;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACTTCAGCTACTCATGCTCCCTAAA 60
|
Db 81 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACTTCAGCTACTCATGCTCCCTAAA 140
|
Qy 61 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 120
|
Db 141 ATGGGCAAACTTTCAGAGCAGCAAAACAGCAACAGCCCTCTGCTGCTGACCTT 200
|
Qy 121 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 154
|
Db 201 GGAGCTGGGGGAGAGTCCAGAGCCTCTCTGGGC 234
|

RESULT 5
AX358722 41907 bp DNA linear PAT 13-FEB-2002

LOCUS

AX358722


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DEFINITION Sequence 100 from Patent WO0190419.
ACCESSION AK358722
VERSION AK358722.1 GI:18675256
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Stanton, V.P.
AUTHORS Methods for genetic analysis of dna to detect sequence variances
TITLE Patent: WO 0190419-A 100 29-NOV-2001;
JOURNAL Variagenics, Inc. (US) ; Stanton, Vincent P., Jr. (US)
FEATURES
source
1. 41907
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 154; DB 6; Length 41907;
Best Local Similarity 100.0%; Pred. No. 1,1e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTGCTGCTCTGAGTCCACTGAAACAACCTGACCTGCTGACCTAA 60
DB 36908 GTTGTGTGCTGCTCTGAGTCCACTGAAACAACCTGACCTGCTGACCTAA 36967
QY 61 ATGGCAACAATTGACAGACAGCAACAACAACAGACCTGCTGCTGACCTT 120
DB 36968 ATGGCAACAATTGACAGACAGCAACAACAACAGACCTGCTGCTGACCTT 37027
QY 121 GGAGCTGGGGCAGAGCTCAGAGACCTCTCTGGGC 154
DB 37028 GGAGCTGGGGCAGAGCTCAGAGACCTCTCTGGGC 37061
RESULT 6
LOCUS APO50154 41907 bp DNA linear PRI 10-MAR-1999
DEFINITION Homo sapiens clone F19374 APO B-C2 gene cluster, complete sequence.
ACCESSION AF050154 AB012576
VERSION AF050154.1 GI:4105701
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 41907)
AUTHORS Freltas, E.M., Zhang, W.J., Lalonde, J.P., Tay, G.K., Gaudieri, S.,
Ashworth, L.K., Van Bockmeer, F.M. and Dawkins, R.L.
TITLE Sequencing of 42kb of the APO B-C2 gene cluster reveals a new gene:
PEREC1
JOURNAL DNA Seq. 9 (2), 89-100 (1998)
PUBMED 10520737
REFERENCE
2 (bases 1 to 41907)
AUTHORS Freltas, E.M. and Zhang, W.J.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-1998) Centre for Molecular Immunology and
Instrumentation, University of Western Australia, PO Box 507,
Subiaco, WA 6008, Australia
3 (bases 1 to 41907)
REFERENCE
1 Stanton, V.P.
AUTHORS Methods for genetic analysis of dna to detect sequence variances
TITLE Patent: WO 0190419-A 100 29-NOV-2001;
JOURNAL Variagenics, Inc. (US) ; Stanton, Vincent P., Jr. (US)
COMMENT
FEATURES
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1. 41907
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.2"
/clone="cosmid F19374"
/note="Sequence was obtained from the shotgun sequencing
of the cosmid clone, F19374. This clone was kindly
provided by the Lawrence Livermore National Laboratories,
CA"
<978. >1250
/gene="PRR2"
<978. >1250
/gene="PRR2"
<978. >1250
/gene="PRR2"
/note="Member of the poliovirus receptor family"
/codon_start=1
/product="poliovirus receptor related protein 2"
/protein_id="AAD02503.1"
/db_xref="GI:4105702"
/translation="QEMPRYHELPTLEBSGPHLPGATSLGSP1PVPGPVAVDSVL
DLRDEBGRREERYLDKINPIYDALSYSSPSDYSGKGFVMSRAMYV"
4000. 16000
/gene="D19S1177E"
join(<4287. 4560,5264. 5331,5708. 5800,6651. 6752,
6832. 6937,13297. 13419,13595. 13671,13775. 13877,
15597. >15736)
/gene="D19S1177E"
/product="D19S1177E"
join(4287. 4560,5264. 5331,5708. 5800,6651. 6752,
6832. 6937,13297. 13419,13595. 13671,13775. 13877,
15597. 15736)
/note="D19S1177E"
/gene="C18B9.6 homolog; Alias: PEREC1"
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/protein_id="AAD02504.1"
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/translation="MGAVLAASSPPAGPPPPALVGLPPPPSPGFTLLPPLGSL
GAGTSSRSRRTPQAAATASAGAAEDACCLPNPGTFFBCHRCXKLFPQWGVK
LTNKGKSNHFOVNHVLAFTIGSNVHFVGTYYGTOLSPTEAFVAVGMDNSGL
NAQVTHQGPRLERKMAICTOOSKPFVMQVNGEFGSFTAAVLTGNDVAVGSGILV
AHYQSLTPCLADGELVTHRRPBBEGVMSLAKYLLTNMLATVTTGGAGMHAITYH
KASDQGVVEREASTRMQTVSFGYQDLPKANLFFKGSVDSNMVIGATLEKCLP
LPITLALGAFIHRKMKFCGFGLTIG"
17311. 22826
/gene="APOB"
/allele="epsilon 3"
join(18364. 18407,19191. 19233,20326. 20518,21099. 21958)
/gene="APOB"
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join(19191. 19233,20326. 20518,21099. 21958)
/gene="APOB"
/allele="epsilon 3"
/db_xref="GI:4105704"
/product="apolipoprotein B"
/protein_id="AAD02505.1"
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/translation="MKYLMALLVYFLAGCOAKYQAVTEPEPELRQOTWOSQRM
ELAGRFVDYLRWQVTLSEVOYBELSQVTOELBALMDETMKELKAYKSLBOLTLP
VAESTRAVLSKELDAQRLGADHEDVCGRLVQVRGAVQMLGOSTELRYLALSLG
KLRRRLADADDLKRLAVYQAGABEGRLSATIRLFGFLVEGRRVRAATVGSILAG
QPLRRQAQNGERLARLAEWESRTRDLDEKGVAVRAKLEBOAQOQIRLOAEAFQ
ARLSWFEPLVEDMQQWAGVYKQVAVGTSAAVPSPDNH"
26780. 32027
/gene="APO C1"
join(<27457. 27514,28755. 28890,31736. >31793)
/gene="APO C1"
join(27457. 27514,28755. 28890,31736. 31793)
/gene="APO C1"
/codon_start=1
/product="apolipoprotein C1"
/protein_id="AAD02506.1"

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/db_xref="GI:4105705"
/translation="MRPLP1,PLVWVLTIVLGGPAPAGCTPDVSSALDKLKEFGNTL
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36828..37547
/ gene="HCR-1"
/ note="Hepatic control region 1"
/pseudo
36828..37547
/ gene="HCR-1"
/ pseudo
CDS
36828..37547
/ gene="HCR-1"
/ pseudo
CDS
36506..>41907
/ gene="APOC1"
/ note="apolipoprotein C1 pseudogene"
/ pseudo
36506..>41907
/ gene="APOC1"
/ pseudo
/ codon_start=1
ORIGIN
Query Match 100.0%; Score 154; DB 8; Length 41907;
Best Local Similarity 100.0%; Pred. No. 1,3e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTGCTCTGAGTCCACACTGAAACAACTTCACTCATGTCCTTAA 60
DB 36908 GTTGTGCTGCTCTGAGTCCACACTGAAACAACTTCACTCATGTCCTTAA 36967
QY 61 ATGGGCAAACTTGCAGACGAAACAGCAACACAGCCCTTCTGCTGACCTT 120
DB 36968 ATGGGCAAACTTGCAGACGAAACAGCAACACAGCCCTTCTGCTGACCTT 37027
QY 121 GGAGCTGGGGCAGAGTCAAGACCTCTCTGGGC 154
DB 37028 GGAGCTGGGGCAGAGTCAAGACCTCTCTGGGC 37061
RESULT 7
AC011481 107567 bp DNA linear PRI 29-MAR-2001
LOCUS AC011481
DEFINITION Homo sapiens chromosome 19 clone CTB-129P6, complete sequence.
ACCESSION AC011481
VERSION AC011481.4 GI:13487947
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 107567)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Direct Submission
JOURNAL Unpublished
TITLE 2 (bases 1 to 107567)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 107567)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Direct Submission
JOURNAL Submitted (29-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
On Mar 29, 2001 this sequence version replaced gi:8576069.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.sngc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.4.
SHGC-11493 GI4568

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FEATURES
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1..107567
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="CTB-129P6"
ORIGIN
Query Match 100.0%; Score 154; DB 8; Length 107567;
Best Local Similarity 100.0%; Pred. No. 1,3e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTGCTCTGAGTCCACACTGAAACAACTTCACTCATGTCCTTAA 60
DB 67169 GTTGTGCTGCTCTGAGTCCACACTGAAACAACTTCACTCATGTCCTTAA 67228
QY 61 ATGGGCAAACTTGCAGACGAAACAGCAACACAGCCCTTCTGCTGACCTT 120
DB 67229 ATGGGCAAACTTGCAGACGAAACAGCAACACAGCCCTTCTGCTGACCTT 67288
QY 121 GGAGCTGGGGCAGAGTCAAGACCTCTCTGGGC 154
DB 67289 GGAGCTGGGGCAGAGTCAAGACCTCTCTGGGC 67322
RESULT 8
AC021988 208239 bp DNA linear HTG 07-JUL-2000
LOCUS AC021988
DEFINITION Homo sapiens chromosome 19 clone RPL1-84C16, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
ACCESSION AC021988
VERSION AC021988.4 GI:8569766
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 208239)
Waterson,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 208239)
Waterson,R.H.
Direct Submission
Submitted (23-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7230864.
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H NH0084C16
----- Summary Statistics -----
Sequencing vector: M13; 95%
Sequencing vector: plasmid; 5%
Chemistry: Dye-terminator Big Dye; 5% of reads
Chemistry: Dye-terminator Big Dye; 5% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 192142 bases at least Q40
Consensus quality: 197519 bases at least Q30
Consensus quality: 200851 bases at least Q20
Insert size: 198000; agarose-fp
Insert size: 206739; sum-of-contigs
Quality coverage: 5.02 in Q20 bases; agarose-fp
Quality coverage: 4.88 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently

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                  /note="assembly_name:Contig13"
gap              1608. 1707
                  /estimated_length=unknown
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                  /note="assembly_name:contig15"
gap             3349. 3448
                  /estimated_length=unknown
misc_feature     3449. 5455
                  /note="assembly_name:Contig16"
gap             5455. 5555
                  /estimated_length=unknown
misc_feature     5555. 7647
                  /note="assembly_name:Contig17"
gap            7648. 7747
                  /estimated_length=unknown
misc_feature     7748. 13438
                  /note="assembly_name:Contig18"
gap            13439. 13538
                  /estimated_length=unknown
misc_feature    13539. 22131
                  /note="assembly_name:Contig19"
gap            22132. 22331
                  /estimated_length=unknown
misc_feature    22332. 29647
                  /note="assembly_name:Contig20"
                  /clone_end=17
                  /vector_side="right"
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ORIGIN

Matches

Dib

Dr

Db

AC146473

ACCESSIO

ORGANIZATIONAL

REFERENCE

JOURNAL

REFERENCE 2 (bases 1 to 39483)
 AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 TITLE Peng, Z., Malinov, I. and Rubin, E.M.
 JOURNAL Submitted (16-AUG-2003) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA

COMMENT
 Sequence Produced by Berkeley PGA
 Web site: <http://pga.lbl.gov>
 Center Code: PGABERK
 Center Project Name: I005
 Bac Clone Name: R2140-83M19

This sequence has been compared to sequences of other species
 using Vista (<http://www-gsd.lbl.gov/VISTA>). The results can be
 viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=nvalue=AP0C2

The order-orientation of the draft sequence was accomplished by
 using:
 Avid (<http://baboon.math.berkeley.edu/avid/>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.

Funding agent: Programs for Genomic Applications (NHLBI)

Summary Statistics:
 Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 22109: contig of 22109 bp in length
 * 22110 22209: gap of unknown length
 * 22210 39483: contig of 17274 bp in length.
 Location/Qualifiers
 1..39483
 /organism="Hylobates klossii"
 /mol_type="genomic DNA"
 /db_xref="taxon:9587"
 /clone="R2140-83M19"
 22110..22209
 gap
 /estimated_length=unknown

ORIGIN
 Query Match 91.7%; Score 141.2; DB 14; Length 39483;
 Best Local Similarity 94.8%; Pred. No. 3.8e-38;
 Matches 146; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTGTGAAGTCAACTGAACAACTTCAGCTACTGATGCTCTAA 60
 Db 31854 GTTGTGTGCTGCTGTGAAGTCAACTGAACAACTTCAGCTACTGATGCTCTAA 31913
 QY 61 ATGGGCAAACTTCGACGACCAACGACCAACACAGCCCTCCCTGCTGCTGACTT 120
 Db 31914 ATGGGCAAACTTCGACGACCAACGACCAACACAGCCCTCCCTGCTGCTGACTT 31973
 QY 121 GGAGCTGGGGGAGAGTCAAGAGACCTCTCTGGGC 154
 Db 31974 GGAGCTGGGGGAGAGTCAAGAGACCTCTCTGGGC 32007

RESULT 10
 AC145523
 LOCUS
 DEFINITION Papio hamadryas clone RP41-112M21, WORKING DRAFT SEQUENCE, 4
 ordered pieces.

ACCESSION AC145523
 VERSION GI:33438604
 KEYWORDS HTGS PHASE2; HTGS DRAFT.
 SOURCE
 ORGANISM
 Papio hamadryas (hamadryas baboon)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecoidea; Papio.

REFERENCE
 AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 TITLE Peng, Z., Malinov, I. and Rubin, E.M.
 JOURNAL Submitted (19-JUL-2003) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 3 (bases 1 to 183798)
 Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 TITLE Peng, Z., Malinov, I. and Rubin, E.M.
 JOURNAL Submitted (05-AUG-2003) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 On Aug 5, 2003 this sequence version replaced gi.32996764.

COMMENT
 Sequence Produced by Berkeley PGA
 Web site: <http://pga.lbl.gov>
 Center Code: PGABERK
 Center Project Name: B056
 Bac Clone Name: RP41-112M21

This sequence has been compared to sequences of other species
 using Vista (<http://www-gsd.lbl.gov/VISTA>). The results can be
 viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=nvalue=AP0C2

The order-orientation of the draft sequence was accomplished by
 using:
 Avid (<http://baboon.math.berkeley.edu/avid/>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.

Funding agent: Programs for Genomic Applications (NHLBI)

Summary Statistics:
 Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 59944: contig of 59944 bp in length
 * 59945 60044: gap of unknown length
 * 60045 168286: contig of 108242 bp in length
 * 168287 168386: gap of unknown length
 * 168387 171995: contig of 3609 bp in length
 * 171996 172095: gap of unknown length
 * 172096 183798: contig of 11703 bp in length.
 Location/Qualifiers
 1..183798
 /organism="Papio hamadryas"
 /mol_type="genomic DNA"
 /db_xref="taxon:9557"
 /clone="RP41-112M21"
 59945..60044
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 /estimated_length=unknown

gap 168287.168386
 gap /estimated_length=unknown
 gap 171996.172095
 gap /estimated_length=unknown

ORIGIN

Query Match 90.6%; Score 139.6; DB 14; Length 183798;
 Best Local Similarity 94.2%; Pred. No. 1.8e-37;
 Matches 145; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 GTTGTGTGCTGCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCCTAA 60
 162213 GTTGTGTGCTGCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCCTAA 162272

61 ATGGCAAAACATTGACAGACAGAAACAGAAACAGACAGCCCTCCCTGCTGACCTT 120
 162273 ATGGCAAAACATTGACAGACAGAAACAGAAACAGACAGCCCTCCCTGCTGACCTT 162332

121 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 154
 162333 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 162366

RESULT 11

AC148222 231234 bp DNA linear HTG 14-FEB-2004
 AC148222 Colobus guereza clone CH272-38C16, WORKING DRAFT SEQUENCE, 8
 ordered pieces.
 AC148222.1 GI:42557404
 HTG, HTGS_PHASE2, HTGS_DRAFT.
 KEYWORDS Colobus guereza (guereza)
 SOURCE Colobus guereza
 ORGANISM Colobus guereza; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Colobinae; Colobus.
 1 (bases 1 to 231234)
 Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 Peng, Z., Malinov, I. and Rubin, S.M.
 Direct Submission
 Unpublished
 2 (bases 1 to 231234)
 Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 Peng, Z., Malinov, I. and Rubin, S.M.
 Direct Submission
 Unpublished
 TITLE Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 JOURNAL Peng, Z., Malinov, I. and Rubin, S.M.
 REFERENCE Direct Submission
 AUTHORS Submitted (14-FEB-2004) Genome Sciences, Lawrence Berkeley National
 JOURNAL Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 COMMENT

Sequence Produced by Berkeley PGA
 Web site: <http://pga.lbl.gov>
 Center Code: PGABERK
 Center Project Name: CLO13
 Bac Clone Name: CH272-38C16

This sequence has been compared to sequences of other species
 using VISTA (<http://www-gsd.lbl.gov/VISTA>). The results can be
 viewed at:
http://pga.lbl.gov/cgi-bin/search_cvsq?type=newvalue=APOC2

The order-orientation of the draft sequence was accomplished by
 using:
 Avid (<http://baboon.math.berkeley.edu/avid/>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.
 Funding agent: Programs for Genomic Applications (NHLBI)

Summary Statistics:
 Sequencing vector: plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly Program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 69606: contig of 69606 bp in length
 * 69607 69706: gap of unknown length
 * 69707 78173: contig of 8467 bp in length
 * 78174 78273: gap of unknown length
 * 78274 110638: contig of 3365 bp in length
 * 110639 110738: gap of unknown length
 * 110739 117542: contig of 6804 bp in length
 * 117543 117642: gap of unknown length
 * 117643 121544: contig of 3902 bp in length
 * 121545 121644: gap of unknown length
 * 121645 163598: contig of 41954 bp in length
 * 163599 163698: gap of unknown length
 * 163699 199977: contig of 36279 bp in length
 * 199978 200077: gap of unknown length
 * 200078 231234: contig of 31157 bp in length.

FEATURES

source
 1..231234
 /organism="Colobus guereza"
 /mol_type="genomic DNA"
 /db_xref="taxon:33548"
 /clone="CH272-38C16"
 69607..69706
 /estimated_length=unknown
 78174..78273
 /estimated_length=unknown
 110639..110738
 /estimated_length=unknown
 117543..117642
 /estimated_length=unknown
 121545..121644
 /estimated_length=unknown
 163599..163698
 /estimated_length=unknown
 199978..200077
 /estimated_length=unknown

ORIGIN

Query Match 88.6%; Score 136.4; DB 14; Length 231234;
 Best Local Similarity 92.9%; Pred. No. 2.5e-36;
 Matches 143; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1 GTTGTGTGCTGCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCCTAA 60
 178100 GTTGTGTGCTGCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCCTAA 178159

61 ATGGCAAAACATTGACAGACAGAAACAGAAACAGACAGCCCTCCCTGCTGACCTT 120
 178160 ATGGCAAAACATTGACAGACAGAAACAGAAACAGACAGCCCTCCCTGCTGACCTT 178219

121 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 154
 178220 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 178253

RESULT 12

HSU35114 4097 bp DNA linear PRI 07-NOV-1996
 LOCUS HsU35114
 DEFINITION Human apolipoprotein B (APOB) gene, hepatic control region HCR-2.
 ACCESSION U35114
 VERSION U35114.1 GI:1049244
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 4097)

AUTHORS	Dang,Q. and Taylor,J.
TITLE	In vivo footprinting analysis of the hepatic control region of the human apolipoprotein E/C-I/C-II gene locus
JOURNAL	J. Biol. Chem. 271 (45), 28667-28676 (1996)
PUBMED	8910501
REFERENCE	2 (bases 1 to 4097)
AUTHORS	Allan,C.M., Walker,D. and Taylor,J.M.
TITLE	Direct Submission
JOURNAL	Submitted (30-AUG-1995) John Taylor, Cardiovascular, Glaxstone Institute, P.O. Box 419100, San Francisco, CA 94141-9100, USA
FEATURES	Location/Qualifiers
source	1..4097
gene	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/note="DNA sequenced was from a P1 plasmid clone from a human genomic library from Genome Systems, Inc., St. Louis, MO;chromosome 19q"
misc_signal	1..4097
	/gene="APOE"
	/gene="APOB"
	/standard_name="HCR-2"
	/function="hepatic control region"
ORIGIN	
Query Match	. 85.5%; Score 131.6; DB 8; Length 4097;
Best Local Similarity	90.9%; Pred. No. 6,7e-35;
Matches 140; Conservative 0; Mismatches 14; Indels 0; Gaps 0	
OY	1 GTTTGTGTCCTCCCTTGAGTTCACATGAACAATTCAAGCCTACTCATGTCCCTAA 60
DB	132 GTTGTGTCCTCCCTCTTAAGTCCACCCTGATATGCCTTCAGCTGTTCCCTCCCTAT 191
OY	61 ATGGGCAACATTTGCACAGACAGAACACAGAGCCCTCGCTGCTGACCTT 120
DB	192 ATGGGCAACATTTGCACAGACAGAACACAGACATATGACCTTCCTGCTGACCTT 251
OY	121 GAAGCTGGGCGAAGCTCAAGACACTCTCTGGGC 154
DB	252 GGAGCTGGCGGAGAAGTCAAGACACTCTCAAGGC 285
RESULT 13	
AC120211/c	63931 bp DNA linear HTG 04-MAY-2002
LOCUS	Pan troglodytes clone RP43-174J24, WORKING DRAFT SEQUENCE, 20
DEFINITION	unordered pieces.
ACCESSION	AC120211 GI:20451083
VERSION	HTG, HTGS, PHASEB1, HTGS, DRAFT.
KEYWORDS	Pan troglodytes (chimpanzee).
SOURCE	Pan troglodytes
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.
REFERENCE	1 (bases 1 to 63931)
AUTHORS	Martin,J.J., Hoseini,R., Peng,Y., Peng,Z., Rubin,E.M. and Cheng,J.-F.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 63931)
AUTHORS	Martin,J.J., Hoseini,R., Peng,Y., Peng,Z., Rubin,E.M. and Cheng,J.-F.
TITLE	Direct Submission
JOURNAL	Submitted (04-MAY-2002) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT	Draft Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABERK Additional information: Comparative analysis and ordering by homology are available here: http://pga.lbl.gov/cgi-bin/search cvcgd?type=newvalue=APOB

	Funding agent: Programs for Genomic Applications (NH&I)
	Contact: 'Jody Schwartz' jrschwartz@lbl.gov
	Summary Statistics
	Sequencing vector: pLacmid, pUC18
	Chemistry: Dye-terminator Big Dye
	Assembly program: Phrap version 0.990329.
	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 20 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.
	*
gap	1 2246: contig of 2246 bp in length
	2247 2246: gap of unknown length
gap	2247 4620: contig of 2274 bp in length
	4621 4720: gap of unknown length
gap	4721 6913: contig of 2192 bp in length
	6913 7012: gap of unknown length
gap	7013 9135: contig of 2123 bp in length
	9136 9235: gap of unknown length
gap	9236 11899: contig of 2664 bp in length
	11899 11999: gap of unknown length
gap	12000 14152: contig of 2153 bp in length
	14153 14252: gap of unknown length
gap	14253 17633: contig of 3381 bp in length
	17634 17733: gap of unknown length
gap	17734 21051: contig of 3318 bp in length
	21052 21151: gap of unknown length
gap	21152 25022: contig of 3871 bp in length
	25023 25122: gap of unknown length
gap	25123 27204: contig of 2082 bp in length
	27205 27304: gap of unknown length
gap	27305 29686: contig of 2382 bp in length
	29687 29786: gap of unknown length
gap	29787 31937: contig of 2151 bp in length
	31938 32037: gap of unknown length
gap	32038 34727: contig of 2690 bp in length
	34728 34827: gap of unknown length
gap	34828 38304: contig of 3477 bp in length
	38305 38404: gap of unknown length
gap	38405 42265: contig of 3861 bp in length
	42266 42365: gap of unknown length
gap	42366 45543: contig of 3178 bp in length
	45544 45643: gap of unknown length
gap	45644 49570: contig of 3927 bp in length
	49571 49670: gap of unknown length
gap	49671 53133: contig of 3463 bp in length
	53134 53233: gap of unknown length
gap	53234 60427: contig of 7194 bp in length
	60428 60527: gap of unknown length
gap	60528 63931: contig of 3404 bp in length.
	Location/Qualifiers
FEATURES	1..63931
source	/organism="Pan troglodytes"
	/mol_type="genomic DNA"
	/db_xref="taxon:9598"
	/clone="RP43-174U24"
gap	2247..2346
	/estimated_length=unknown
gap	4621..4720
	/estimated_length=unknown
gap	6913..7012
	/estimated_length=unknown
gap	9136..9235
	/estimated_length=unknown
gap	11900..11999
	/estimated_length=unknown
gap	14153..14252
	/estimated_length=unknown
gap	17634..17733
	/estimated_length=unknown


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gap      21052..21151
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gap      25023..25122
          /estimated_length=unknown
gap      27205..27304
          /estimated_length=unknown
gap      29687..29786
          /estimated_length=unknown
gap      31938..32037
          /estimated_length=unknown
gap      34728..34827
          /estimated_length=unknown
gap      38305..38404
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gap      42266..42365
          /estimated_length=unknown
gap      45544..45643
          /estimated_length=unknown
gap      49571..49670
          /estimated_length=unknown
gap      53134..53233
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gap      60428..60527
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ORIGIN
Query Match      85.5%; Score 131.6; DB 14; Length 63931;
Best Local Similarity 90.3%; Pred. No. 1e-34;
Matches 140; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      1 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACCTTCAAGCCCTACATGATGCTCTAA 60
Db      3331 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACCTTCAAGCCCTACATGATGCTCTAA 3272

Qy      61 ATGGGCAACATTGACAGCAGCAACAGCAACAGCAGCCCTCCCTGCTGCTGACCTT 120
Db      3271 ATGGGCAACATTGACAGCAGCAACAGCAACAGCAGCCCTCCCTGCTGCTGACCTT 3212

Qy      121 GGAGCTGGGGGCAAGAGTCAAGAGACTCTCTGCGGC 154
Db      3211 GGAGCTGGGGGCAAGAGTCAAGAGACTCTCTGCGGC 3178

RESULT 14
AC145523      183798 bp      DNA      linear      HTG 05-AUG-2003
LOCUS      Papiio hamadryas clone RP41-112M21, WORKING DRAFT SEQUENCE, 4
DEFINITION      ordered pieces.
ACCESSION      AC145523
VERSION      AC145523.2 GI:33438604
KEYWORDS      HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE      Papiio hamadryas (hamadryas baboon)
ORGANISM      Papiio hamadryas
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecoidea; Cercopithecinae; Papio.
REFERENCE      1 (bases 1 to 183798)
            Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
            Peng, Z., Malinov, I. and Rubin, E.M.
            Direct Submission
            Unpublished
            2 (bases 1 to 183798)
            Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
            Peng, Z., Malinov, I. and Rubin, E.M.
            Direct Submission
            Submitted (19-JUN-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
            3 (bases 1 to 183798)
            Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
            Peng, Z., Malinov, I. and Rubin, E.M.
            Direct Submission
            Submitted (05-AUG-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA

```

COMMENT

On Aug 5, 2003 this sequence version replaced gi:32996764.

Sequence Produced by Berkeley PG
 Web site: <http://pga.lbl.gov>
 Center Code: PGABERK
 Center Project Name: B056
 Bac Clone Name: RP41-112M21

This sequence has been compared to sequences of other species using VISTA (<http://www-gsd.lbl.gov/VISTA>). The results can be viewed at:
http://pga.lbl.gov/cgi-bin/search_cwcd?type=ncvalue-APOC2

The order-orientation of the draft sequence was accomplished by using:
 Avid (<http://baboon.math.berkeley.edu/avid/>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.

Funding agent: Programs for Genomic Applications (NH&M)

Summary Statistics:

Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly Program: Phrap version 0.990329. It currently
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 59944: contig of 59944 bp in length
 * 59945 60044: gap of unknown length
 * 60045 168286: contig of 108242 bp in length
 * 168287 168386: gap of unknown length
 * 168387 171995: contig of 3609 bp in length
 * 171996 172095: gap of unknown length
 * 172096 183798: contig of 11703 bp in length.

FEATURES

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 /mol_type="genomic DNA"
 /db_xref="taxon:9557"
 /clone="RP41-112M21"
 59945..60044
 /estimated_length=unknown
 168287..168386
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 171996..172095
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ORIGIN

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Query Match      84.4%; Score 130; DB 14; Length 183798;
Best Local Similarity 90.3%; Pred. No. 4.4e-34;
Matches 139; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy      1 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACCTTCAAGCCCTACATGATGCTCTAA 60
Db      67062 GTTGTGTGCTGCTCTGAAGTCCAGACTGAACAACCTTCAAGCCCTACATGATGCTCTAA 67003

Qy      61 ATGGGCAACATTGACAGCAGCAACAGCAACAGCAGCCCTCCCTGCTGCTGACCTT 120
Db      67002 ATGGGCAACATTGACAGCAGCAACAGCAACAGCAGCCCTCCCTGCTGCTGACCTT 66943

Qy      121 GGAGCTGGGGGCAAGAGTCAAGAGACTCTCTGCGGC 154
Db      66942 GGAAGCTGGGGGCAAGAGTCAAGAGACTCTCTGCGGC 66909

RESULT 15
AC146285

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LOCUS AC146285 185724 bp DNA linear HTG 07-AUG-2003
 DEFINITION Callicebus moloch clone LBS-404K13, WORKING DRAFT SEQUENCE, 6
 ordered pieces.
 ACCESSION AC146285.2 GI:33469171
 VERSION AC146285
 KEYWORDS HTG, HTGS PHASE2, HTGS DRAFT.
 SOURCE Callicebus moloch (Dusky titi)
 ORGANISM Callicebus moloch
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buthera; Euarchontoglires; Primates; Platyrrhini;
 Cebidae; Callicebinae; Callicebus.
 REFERENCE 1 (bases 1 to 185724)
 AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 Peng, Z., Malinov, I. and Rubin, E.M.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 185724)
 AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 Peng, Z., Malinov, I. and Rubin, E.M.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2003) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 REFERENCE 3 (bases 1 to 185724)
 AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
 Peng, Z., Malinov, I. and Rubin, E.M.
 TITLE Direct Submission
 JOURNAL Submitted (07-AUG-2003) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 COMMENT On Aug 7, 2003 this sequence version replaced GI:33413350.
 Sequence Produced by Berkeley PGA
 Web site: <http://pga.lbl.gov>
 Center Code: PGABRRK
 Center Project Name: T019
 Bac Clone Name: LBS-404K13
 This sequence has been compared to sequences of other species
 using VISTA (<http://www-gsd.lbl.gov/VISTA>). The results can be
 viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgdt?value=NAvalue=APCC2
 The order-orientation of the draft sequence was accomplished by
 using:
 Avid (<http://baboon.math.berkeley.edu/avid/>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.
 Funding agent: Programs for Genomic Applications (NHBLI)
 If the Bac library Name is LBI to LB4, please see website
 for the description: <http://www-gsd.lbl.gov/cheng/BAC.html>
 These libraries are available through the BACPAC Resources Center:
<http://www.chori.org/bacpac/libraries.htm> as LBNL-1 to LBNL-4.
 Summary Statistics:
 Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1
 * 6537 6536: gap of 6536 bp in length
 * 6637 54159: contig of 47523 bp in length
 * 54160 54259: gap of unknown length
 * 54260 76479: contig of 22220 bp in length
 * 76480 76579: gap of unknown length
 * 76580 110159: contig of 33580 bp in length

FEATURES
 SOURCE
 * 110160 110259: gap of unknown length
 * 110260 133023: contig of 22764 bp in length
 * 133024 133123: gap of unknown length
 * 133124 185724: contig of 52601 bp in length.
 Location/Qualifiers
 1. 185724
 /organism="Callicebus moloch"
 /mol_type="genomic DNA"
 /db_xref="taxon:9523"
 /clone="LBS-404K13"
 6537..6636
 /estimated_length=unknown
 54160..54259
 /estimated_length=unknown
 76480..76579
 /estimated_length=unknown
 110160..110259
 /estimated_length=unknown
 133024..133123
 /estimated_length=unknown
 ORIGIN
 Query Match 74.3%; Score 114.4; DB 14; Length 185724;
 Best Local Similarity 87.3%; Pred. No. 1.4e-28;
 Matches 138; Conservative 0; Mismatches 16; Indels 4; Gaps 1;
 Oy 1 GTTTGTGTCGCTCTGAAGTCACAGCAAACTGAGCTTCAATGCTCTAA 60
 Db 148042 GTTTCGTCGCTCTGAGTCAAGTCAAGCACTTCAAGCTTCTCTCTCTGAG 148101
 Oy 61 ATGGGCAAACTTTCAGG---CAGCAAAAGCAAAAGCAAGGCTCTCTGCTCTGA 116
 Db 148102 ATGGGCAAACTTTCAGGCAAAAGCAAAAGCAAGGCAAGGCTCTCTGCTCTGA 148161
 Oy 117 CCTTGAAGCTGGGGCAGAGGCTCAAGAGCTCTCTCTGGGC 154
 Db 148162 CCTGGAGCTGGGGCAGAGGCTCAAGAGCTCTCTCTGGGC 148199

Search completed: April 18, 2006, 14:56:52
 Job time : 848.062 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 18, 2006, 12:03:10 ; Search time 93.4261 Seconds
(without alignments)
10985.822 Million cell updates/sec

Title: US-09-884-901a-8

Perfect score: 154
Sequence: 1 gttctgctgcctgcctcga.....gttcagagacctctcgtg99c 154

Scoring table: IDENTITY NUC
Gapop 10'-0', Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: geneeqn1980s:*
- 2: geneeqn1900s:*
- 3: geneeqn2000s:*
- 4: geneeqn2001as:*
- 5: geneeqn2001bs:*
- 6: geneeqn2002as:*
- 7: geneeqn2002bs:*
- 8: geneeqn2003as:*
- 9: geneeqn2003bs:*
- 10: geneeqn2003cs:*
- 11: geneeqn2003ds:*
- 12: geneeqn2004as:*
- 13: geneeqn2004bs:*
- 14: geneeqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	100.0	154	AAI71009	AAI71009 Human apo
2	154	100.0	328	AAI71010	AAI71010 Human apo
3	154	100.0	771	AAI71005	AAI71005 Human apo
4	154	100.0	774	AAQ92616	AAQ92616 Human hep
5	154	100.0	1079	ABE31916	ABE31916 Human Apo
6	151	98.1	154	ABV73262	ABV73262 Apolipop
7	82	53.2	90	AAV19597	AAV19597 Apolipop
8	82	53.2	90	AAV19583	AAV19583 Apolipop
9	82	53.2	90	AAV15382	AAV15382 Apolipop
10	82	53.2	90	AAV15386	AAV15386 Apolipop
11	82	53.2	90	ADU47587	ADU47587 Oligonuc
12	82	53.2	90	ADU47583	ADU47583 Oligonuc
13	78	50.6	82	AAV19599	AAV19599 Apolipop
14	78	50.6	82	ADU47589	ADU47589 Apolipop
15	77	50.0	82	AAV19585	AAV19585 Apolipop
16	77	50.0	82	ADU47585	ADU47585 Oligonuc
17	76.4	49.6	82	AAV15388	AAV15388 Apolipop
18	75.4	49.0	82	AAV15384	AAV15384 Apolipop
19	74	48.1	78	AAV19596	AAV19596 Apolipop

C 20	74	48.1	78	2	AAV19600	AAV19600 Apolipop
C 21	74	48.1	78	2	AAV15385	AAV15385 Apolipop
C 22	74	48.1	78	13	ADU47590	ADU47590 Oligonuc
C 23	74	48.1	78	13	ADU47586	ADU47586 Oligonuc
C 24	72.4	47.0	78	2	AAV15389	AAV15389 Apolipop
C 25	70	45.5	70	2	AAV15387	AAV15387 Apolipop
C 26	70	45.5	70	2	AAV15387	AAV15387 Apolipop
C 27	70	45.5	70	13	ADU47588	ADU47588 Oligonuc
C 28	69	44.8	70	2	AAV19594	AAV19594 Apolipop
C 29	69	44.8	70	2	AAV15383	AAV15383 Apolipop
C 30	69	44.8	70	13	ADU47584	ADU47584 Oligonuc
C 31	32	20.8	2235	11	ADG73536	ADG73536 Human CDN
C 32	32	20.5	1179	10	ADG73621	ADG73621 Human CDN
C 33	31.6	20.4	88191	8	ABX14763	ABX14763 Genomic D
C 34	31.2	20.3	257	4	ABA75079	ABA75079 Human Ioe
C 35	31.2	20.3	257	4	AAI55613	AAI55613 Probe #24
C 36	31.2	20.3	257	4	ABA39763	ABA39763 Probe #18
C 37	31.2	20.3	257	4	AAK49722	AAK49722 Human bon
C 38	31.2	20.3	257	4	AAK23594	AAK23594 Human bra
C 39	31.2	20.3	257	4	ABE49348	ABE49348 Human liv
C 40	31.2	20.3	257	6	ABE23212	ABE23212 Human gen
C 41	31.2	20.3	567	4	ABA62558	ABA62558 Human fce
C 42	31.2	20.3	567	4	AAI42544	AAI42544 Probe #11
C 43	31.2	20.3	567	4	ABA29886	ABA29886 Probe #83
C 44	31.2	20.3	567	4	AAK36772	AAK36772 Human bon
C 45	31.2	20.3	567	4	AAK10914	AAK10914 Human bra

ALIGNMENTS

RESULT 1	AAI71009	standard; DNA; 154 BP.
ID	AAI71009	standard; DNA; 154 BP.
XX	AAI71009;	
XX	18-MAR-2002 (first entry)	
XX	Human apolipoprotein B gene enhancer.	
XX	Human apolipoprotein B; Apol; enhancer; human; expression cassette; liver;	
XX	Factor IX; blood clotting; gene therapy; ds.	
OS	Homo sapiens.	
XX	WO200198482-A2.	
XX	27-DEC-2001.	
XX	19-JUN-2001; 2001WO-US019634.	
XX	20-JUN-2000; 2000US-0212902P.	
XX	(STRD) UNIV LELAND STANFORD JUNIOR.	
XX	(UNITW) UNIV WASHINGTON.	
XX	Miao CH, Kay MA;	
XX	WPI; 2002-114582/15.	
XX	Nucleic acid construct for expressing nucleic acid molecules, proteins in	
XX	mammalian liver cells, has operably linked hepatic locus control element,	
XX	hepatic promoter, coding sequence, polyadenylation signal and intron.	
XX	Example 2; Page 59; 64p; English.	
XX	The present sequence is that of an enhancer sequence from the human	
XX	apolipoprotein B gene. The enhancer may be incorporated into expression	
XX	cassettes of the invention designed for liver-specific expression of	
XX	Factor IX. The cassettes also include an hepatic locus control region,	
XX	located 5' to a liver-specific promoter, a Factor IX coding sequence, a	
XX	3' polyadenylation signal, and an intron (see AAI71003-16). Also provided	

are vectors that include an expression cassette of the invention. These CC
CC may episomal or integrating vectors, including viral vectors, and are CC
CC used in a claimed method of ameliorating the symptoms of a disease. A CC
CC therapeutic amount of blood clotting Factor IX is produced in mammalian CC
CC liver cells for at least 100, and preferably at least 500, days. In CC
CC examples of the invention, human Factor IX was expressed in mouse liver CC
CC cells following injection of retrovirus-based plasmids that carried the CC
CC expression cassettes into the tail vein or portal vein, and by direct CC
CC injection of plasmid DNA into the liver

XX SQ Sequence 154 BP; 40 A; 47 C; 36 G; 31 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 7,1e-40;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTGTGTGCTGCTCTGTAAGTCACTGAACAATTGAGCTTACTGATGCTCTTAA 60
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DB 1 GTTGTGTGCTGCTCTGTAAGTCACTGAACAATTGAGCTTACTGATGCTCTTAA 60
QY 61 ATGGGCAAACTTGGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 120
    |||
DB 61 ATGGGCAAACTTGGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 120
QY 121 GGAGCTGGGGGAGAGGTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 154
    |||
DB 121 GGAGCTGGGGGAGAGGTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 154
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RESULT 2

AA171010

ID AA171010 standard; DNA; 328 BP.

XX AA171010;

DT 18-MAR-2002 (first entry)

XX Human apolipoprotein B gene hepatic locus control element.

DE Apolipoprotein B; Apob; hepatic locus control element; human;

KM expression cassette; liver; Factor IX; blood clotting; gene therapy; ds.

XX Homo sapiens.

OS WO200198482-A2.

XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-US019634.

XX 20-JUN-2000; 2000US-0212902P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

PA (UNIW) UNIV WASHINGTON.

XX Miao CH, Kay MA;

XX WPI; 2002-114582/15.

XX Nucleic acid construct for expressing nucleic acid molecules, proteins in
XX mammalian liver cells, has operably linked hepatic locus control element,
XX hepatic promoter, coding sequence, polyadenylation signal and intron.

XX Example 2; Page 59; 64pp; English.

XX The present sequence is that of the hepatic locus control element of the
XX human apolipoprotein B gene. The sequence can be incorporated into
XX expression cassettes of the invention designed for liver-specific
XX expression of Factor IX. The cassettes also include an hepatic promoter
XX located 3' to the hepatic locus control element, the Factor IX coding
XX sequence, a 3' polyadenylation signal, and an intron located 3' to the
XX hepatic promoter and 5' to the polyadenylation signal (see AA171003-16).
XX The hepatic locus control element confers copy number dependent, position

independent gene expression. Also provided are vectors that include an CC
CC expression cassette of the invention. These may episomal or integrating CC
CC vectors, including viral vectors. They are used in a claimed method of CC
CC ameliorating the symptoms of a disease. A therapeutic amount of blood CC
CC clotting Factor IX is produced in mammalian liver cells for a period of CC
CC at least 100 days, and preferably at least 500 days. In examples of the CC
CC invention, human Factor IX was expressed in mouse liver cells following CC
CC injection of retrovirus-based plasmids carrying the expression cassettes CC
CC into the tail vein or portal vein, and by direct injection of plasmid DNA CC
CC into the liver

XX SQ Sequence 328 BP; 72 A; 104 C; 84 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 328;

Best Local Similarity 100.0%; Pred. No. 9,3e-40;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GTTGTGTGCTGCTCTGTAAGTCACTGAACAATTGAGCTTACTGATGCTCTTAA 60
    |||
DB 78 GTTGTGTGCTGCTCTGTAAGTCACTGAACAATTGAGCTTACTGATGCTCTTAA 137
QY 61 ATGGGCAAACTTGGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 120
    |||
DB 138 ATGGGCAAACTTGGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 197
QY 121 GGAGCTGGGGGAGAGGTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 154
    |||
DB 198 GGAGCTGGGGGAGAGGTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 231
```

RESULT 3

AA171005

ID AA171005 standard; DNA; 771 BP.

XX AA171005;

DT 18-MAR-2002 (first entry)

XX Human apolipoprotein B Apob-HCR gene hepatic locus control element.

DE Apolipoprotein B; Apob-HCR; hepatic locus control element; human;

KM expression cassette; liver; Factor IX; blood clotting; gene therapy; ds.

XX Homo sapiens.

OS WO200198482-A2.

XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-US019634.

XX 20-JUN-2000; 2000US-0212902P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

PA (UNIW) UNIV WASHINGTON.

XX Miao CH, Kay MA;

XX WPI; 2002-114582/15.

XX Nucleic acid construct for expressing nucleic acid molecules, proteins in
XX mammalian liver cells, has operably linked hepatic locus control element,
XX hepatic promoter, coding sequence, polyadenylation signal and intron.

XX Claim 7; Page 56-57; 64pp; English.

XX The present sequence is that of the hepatic locus control element of the
XX human apolipoprotein B gene, Apob-HCR. The sequence can be incorporated
XX into expression cassettes of the invention designed for liver-specific
XX expression of Factor IX. The cassettes also include an hepatic promoter
XX located 3' to the hepatic locus control element, the Factor IX coding
XX sequence, a 3' polyadenylation signal, and an intron located 3' to the
XX hepatic promoter and 5' to the polyadenylation signal (see AA171003-16).
XX The hepatic locus control element confers copy number dependent, position

CC The hepatic locus control element confers copy number dependent, position
CC independent gene expression. Also provided are vectors that include an
CC expression cassette of the invention. These may be episomal or integrating
CC vectors, including viral vectors. They are used in a claimed method of
CC ameliorating the symptoms of a disease. A therapeutic amount of blood
CC clotting factor IX is produced in mammalian liver cells for a period of
CC at least 100 days, and preferably at least 500 days. In examples of the
CC invention, human factor IX was expressed in mouse liver cells following
CC injection of retrovirus-based plasmids carrying the expression cassettes
CC into the tail vein or portal vein, and by direct injection of plasmid DNA
CC into the liver

XX Sequence 771 BP, 165 A; 215 C; 186 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 771;

Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTGTGTCGCTCTGAAGTCCAGCTGAACAACTTCAAGCCCTCACTGATGTCCTTAA 60

DB 78 GTTTGTGTCGCTCTGAAGTCCAGCTGAACAACTTCAAGCCCTCACTGATGTCCTTAA 137

QY 61 ATGGGCAAACTTGCAGAGCAAGCAACAGACAGCCCTCCCTGCTGACCTT 120

DB 138 ATGGGCAAACTTGCAGAGCAAGCAACAGACAGCCCTCCCTGCTGACCTT 197

QY 121 GGAGCTGGGGGCAAGAGTCAAGAGACCTCTCTGGGC 154

DB 198 GGAGCTGGGGGCAAGAGTCAAGAGACCTCTCTGGGC 231

RESULT 4

AA092616 ID AA092616 standard; DNA; 774 BP.

XX AA092616;

DT 19-DEC-1995 (first entry)

XX Human hepatocyte-specific control region.

XX Human hepatocyte-specific control region; human afamin; HCR enhancer;

XX promoter; transgene; transgenic animal;

XX in vivo system for disease analysis; liver expression; ds.

XX Homo sapiens.

XX WO9511308-A1.

XX 27-APR-1995.

XX 13-OCT-1994; 94WO-US011675.

XX 18-OCT-1993; 93US-00141322.

XX 31-MAR-1994; 94US-00221767.

XX (AMGB-) AMGEN INC.

XX Simonet WS, Lichenstein HS, Lyons DE;

XX WPI; 1995-170228/22.

XX Nucleic acid sequence for liver specific expression of a transgene -

XX comprises hepatocyte specific control region linked to a promoter and the

XX transgene, and is used for the prodn. of a transgenic mammal.

XX Claim 1; Fig 1; 73pp; English.

XX AA092616 is the human hepatocyte-specific control region (HCR enhancer),

XX which was operably linked to a promoter and a transgene, i.e. AA092617

XX which encodes AAR75655, human afamin. The resultant sequence can then be

XX used in the construction of a transgenic mammal, which can produce

XX recombinant afamin, the expression of which may be specific to the liver

CC of the mammal. The mammal may be used as an in vivo system to analyse the

XX course of a disease

XX Sequence 774 BP, 165 A; 214 C; 189 G; 206 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 154; DB 2; Length 774;

Best Local Similarity 100.0%; Pred. No. 1.3e-39;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTGTGTCGCTCTGAAGTCCAGCTGAACAACTTCAAGCCCTCACTGATGTCCTTAA 60

DB 81 GTTTGTGTCGCTCTGAAGTCCAGCTGAACAACTTCAAGCCCTCACTGATGTCCTTAA 140

QY 61 ATGGGCAAACTTGCAGAGCAAGCAACAGACAGCCCTCCCTGCTGACCTT 120

DB 141 ATGGGCAAACTTGCAGAGCAAGCAACAGACAGCCCTCCCTGCTGACCTT 200

QY 121 GGAGCTGGGGGCAAGAGTCAAGAGACCTCTCTGGGC 154

DB 201 GGAGCTGGGGGCAAGAGTCAAGAGACCTCTCTGGGC 234

RESULT 5

ABL31916 ID ABL31916 standard; DNA; 1079 BP.

XX ABL31916;

DT 22-MAR-2002 (first entry)

XX Human Apob genomic partial sequence (36601 to 37680).

XX Genetic analysis; sequence variant detection; genotype; Apob; SNP;

XX single nucleotide polymorphism; polymorphic site; atherosclerosis;

XX dementia; Parkinson's disease; Huntington's disease; PCR primer;

XX neurodegenerative disease; gene; ds.

XX Homo sapiens.

XX WO200190419-A2.

XX 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US016577.

XX 23-MAY-2000; 2000US-0206613P.

XX 25-OCT-2000; 2000US-00686998.

XX 25-OCT-2000; 2000US-00697013.

XX 25-OCT-2000; 2000US-00697028.

XX (VARI-) VARIGENICS INC.

XX (STAN/) STANTON V P.

XX Stanton VP;

XX WPI; 2002-097670/13.

XX Determining the haplotype of at least one allele of a selected gene at

XX two or more polymorphic sites, for assessing disease risk, comprises

XX allele-specific enrichment, optical mapping, or atomic force microscopy.

XX Disclosure; Page 103; 166pp; English.

XX The present invention describes a method for determining the haplotype of

XX an allele of a selected gene at two or more polymorphic sites comprising

XX allele-specific enrichment, optical mapping, or atomic force microscopy.

XX The method is useful for genetic analysis when the DNA segment being

XX haplotyped consists of polymorphisms that are in some degree of linkage

XX disequilibrium with each other, that is they do not assort randomly in

XX the population being studied. The method allows early implementation of

XX preventive measures in patients at risk of diseases such as

XX atherosclerosis, dementia, Parkinson's disease, Huntington's disease or

XX other organic or vascular neurodegenerative diseases. Genotype and

CC haplotype information can be used to make diagnostic tests useful for
 CC disease risk assessment, for prognostic prediction of the course or
 CC outcome of a disease, to diagnose a disease or condition, or to select an
 CC optimal therapy for a disease or condition. ABJ31915 to ABJ32035
 CC represent nucleotide sequence used in the exemplification of the present
 CC invention

SO Sequence 1079 BP; 247 A; 284 C; 286 G; 262 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 1079;
 Best Local Similarity 100.0%; Pred. No. 1.4e-39;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCACTCATGTCCCTTAA 60
 DB 308 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCACTCATGTCCCTTAA 367
 OY 61 ATGGGCAAACTTTCAGAGCAACAGCAAAACAGAGCCCTCTGCTGACCTT 120
 DB 368 ATGGGCAAACTTTCAGAGCAACAGCAAAACAGAGCCCTCTGCTGACCTT 427
 OY 121 GGAGCTGGGGGCAAGGTGACAGACCTCTCTGGC 154
 DB 428 GGAGCTGGGGGCAAGGTGACAGACCTCTCTGGC 461

RESULT 6

ABV73262
 ID ABV73262 standard; DNA; 154 BP.

AC ABV73262;

DT 22-JAN-2003 (first entry)

XX Apolipoprotein B locus control region nucleotide sequence.

XX Adeno-associated virus; AAV; virion; helper virus; secretory gland;
 KM transduction; haemostatic; gene therapy; blood coagulation; haemophilia;
 KM gene transfer; apolipoprotein B; Apob; ds.

XX Unidentified.

XX WO200271843-A1.

XX 19-SEP-2002.

XX 14-MAR-2002; 2002WO-US008350.

XX 14-MAR-2001; 2001US-0275908P.

XX (AVIG-) AVIGEN INC.

XX McCelland A, Scolley R;

XX WPI; 2002-698779/75.

XX Delivering a protein to a mammal, useful in gene transfer, comprises
 PT contacting recombinant adeno-associated virus virions free of helper
 PT virus and having heterologous gene encoding a protein, with a duct of a
 PT secretory gland of mammal.

XX Example 1; Page 32; 48pp; English.

XX The invention relates to delivering a protein to a mammal that involves
 CC contacting recombinant adeno-associated virus (rAAV) virions, which are
 CC free of helper virus, and comprises heterologous gene encoding a protein,
 CC with a duct of a secretory gland of mammal resulting in the transduction
 CC of at least one cell of the secretory gland. The rAAV virion comprising a
 CC heterologous gene is useful in the manufacture of a medicament for
 CC delivery to a duct of a salivary gland, secretory gland or liver of a
 CC mammal. The rAAV virion comprising a gene encoding a blood coagulation
 CC protein may also be used in the manufacture of a medicament for treating
 CC hemophilia. The method is useful in gene transfer, and to facilitate

CC pharmaco- or toxico-kinetic studies. The present sequence represents an
 CC apolipoprotein B (Apob) locus control region nucleotide sequence

XX Sequence 154 BP; 40 A; 47 C; 35 G; 32 T; 0 U; 0 Other;

SO Query Match 98.1%; Score 151; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 6.7e-39;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCACTCATGTCCCTTAA 60
 DB 4 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCACTCATGTCCCTTAA 63
 OY 61 ATGGGCAAACTTTCAGAGCAACAGCAAAACAGAGCCCTCTGCTGACCTT 120
 DB 64 ATGGGCAAACTTTCAGAGCAACAGCAAAACAGAGCCCTCTGCTGACCTT 123
 OY 121 GGAGCTGGGGGCAAGGTGACAGACCTCTCTG 151
 DB 124 GGAGCTGGGGGCAAGGTGACAGACCTCTCTG 154

RESULT 7

AAV19597
 ID AAV19597 standard; DNA; 90 BP.

XX AAV19597;

DT 25-MAR-2003 (revised)

DT 06-AUG-1998 (first entry)

XX Apolipoprotein B (Apo B) enhancer sequence generating sense primer 3.

XX Replication defective; recombinant retrovirus; RRV; therapeutic protein;
 KM haemophilia; thrombosis; hypercoagulable disorder; liver disease;
 KM hepatitis; thalassemia; phenylketonuria; Leach-Nyman syndrome; human;
 KM cystic fibrosis; Duchenne's muscular dystrophy; hypercholesterolemia;
 KM diabetes; hypopituitarism; adenine deaminase deficiency; HIV infection;
 KM anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;
 KM autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein B; Apo B;
 KM enhancer sequence; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9800541-A2.

XX 08-JAN-1998.

XX 02-JUL-1997; 97WO-US011784.

XX 03-JUL-1996; 96US-00645601.

XX 13-AUG-1996; 96US-00696381.

XX 04-JUN-1997; 97US-00869309.

XX (CHIR) CHIRON CORP.

XX Jolly DJ, Barber JR, Chang SMW, Respass JG, Allen JR, Boder M,
 PI Chong K, De la Vega D, Depolo NJ, Hsu DC, Ibanez CB;
 PI Mitelstaedt DM, Prussek CB, Greengard J, Lee R;
 PI WPI; 1998-086966/08.

XX New replication defective recombinant retro-viruses - which can be
 PT administered to provide long term systemic expression of therapeutic
 PT protein in blood, useful in, e.g. treating hyper-coagulable disorders.

XX Example 33; Page 178; 272pp; English.

XX This primer is used for generating the apolipoprotein B (Apo B) enhancer
 CC sequence. This is used to construct a retroviral vector backbone with a
 CC liver specific promoter. The invention provides the preparation of
 CC replication defective recombinant retrovirus (RRV) expressing a

CC therapeutic protein. The RRV preparation is resistant to degradation by
 CC human complement and is capable of inducing long term systemic expression
 CC of the therapeutic protein when administered intravenously to a human.
 CC The long term systemic expression results in a measurable level of the
 CC therapeutic protein being produced in the blood of the human for a period
 CC of at least 30 days after the administration of the RRV vector
 CC preparation. The RRV's can be used for in vivo delivery of therapeutic
 CC protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,
 CC hypercoagulable disorders, liver diseases such as hepatitis, disorders
 CC such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe
 CC combined immunodeficiency (SCID), cystic fibrosis, Duchenne's Muscular
 CC dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,
 CC hypopituitarism, adenine deaminase deficiency, alpha-antitrypsin
 CC deficiency, Gaucher's syndrome, anaemia, infections such as HIV
 CC infection, high blood pressure, Alzheimer's disease, autoimmune or
 CC inflammatory disease or graft versus host disease. RRV's are capable of
 CC surviving inactivation in human serum thereby allowing efficient gene
 CC transfer over prolonged periods of time. (Updated on 25-MAR-2003 to
 CC correct PI field.)

CC Sequence 90 BP; 25 A; 25 C; 17 G; 23 T; 0 U; 0 Other;

Query Match 53.2%; Score 82; DB 2; Length 90;

Best Local Similarity 100.0%; Pred. No. 1,4e-16; Mismatches 0; Indels 0; Gaps 0;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 GTTGTGCTGCTCTGAAGTCCACTGAACAACCTTCCCTACTCATGTCCTTAA 60

CC 9 GTTGTGCTGCTCTGAAGTCCACTGAACAACCTTCCCTACTCATGTCCTTAA 68

CC 61 ATGGGCAAACTTGCAGACG 82

CC 69 ATGGGCAAACTTGCAGACG 90

CC Db

CC AAV19593 standard; DNA; 90 BP.

CC AAV19593;

CC 25-MAR-2003 (revised)

CC 06-AUG-1998 (first entry)

CC Apolipoprotein E (Apo E) enhancer sequence generating sense primer 1.

CC Replication defective; recombinant retrovirus; RRV; therapeutic protein;

CC haemophilia; thrombosis; hypercoagulable disorder; liver disease;

CC hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human;

CC cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemia;

CC diabetes; hypopituitarism; adenine deaminase deficiency; HIV infection;

CC anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;

CC autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein E; Apo E;

CC enhancer sequence; PCR primer; ss.

CC Synthetic.

CC Homo sapiens.

CC WO9800541-A2.

CC 08-JAN-1998.

CC 02-JUL-1997; 97WO-US011784.

CC 03-JUL-1996; 96US-00645601.

CC 13-AUG-1996; 96US-00696381.

CC 04-JUN-1997; 97US-00869309.

CC (CHIR) CHIRON CORP.

XX WPI; 1998-086966/08.

XX New replication defective recombinant retro-viruses - which can be

XX administered to provide long term systemic expression of therapeutic

XX protein in blood, useful in, e.g. treating hyper-coagulable disorders.

XX Example 33; Page 177; 272pp; English.

XX This primer is used for generating the apolipoprotein E (Apo E) enhancer

XX sequence. This is used to construct a retroviral vector backbone with a

XX liver specific promoter. The invention provides the preparation of

XX replication defective recombinant retrovirus (RRV) expressing a

XX therapeutic protein. The RRV preparation is resistant to degradation by

XX human complement and is capable of inducing long term systemic expression

XX of the therapeutic protein when administered intravenously to a human.

XX The long term systemic expression results in the blood of the human for a period

XX of at least 30 days after the administration of the RRV vector

XX preparation. The RRV's can be used for in vivo delivery of therapeutic

XX protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,

XX hypercoagulable disorders, liver diseases such as hepatitis, disorders

XX such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe

XX combined immunodeficiency (SCID), cystic fibrosis, Duchenne's Muscular

XX dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,

XX hypopituitarism, adenine deaminase deficiency, alpha-antitrypsin

XX deficiency, Gaucher's syndrome, anaemia, infections such as HIV

XX infection, high blood pressure, Alzheimer's disease, autoimmune or

XX inflammatory disease or graft versus host disease. RRV's are capable of

XX surviving inactivation in human serum thereby allowing efficient gene

XX transfer over prolonged periods of time. (Updated on 25-MAR-2003 to

XX correct PI field.)

XX Sequence 90 BP; 24 A; 25 C; 18 G; 23 T; 0 U; 0 Other;

Query Match 53.2%; Score 82; DB 2; Length 90;

Best Local Similarity 100.0%; Pred. No. 1,4e-16; Mismatches 0; Indels 0; Gaps 0;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 GTTGTGCTGCTCTGAAGTCCACTGAACAACCTTCCCTACTCATGTCCTTAA 60

CC 9 GTTGTGCTGCTCTGAAGTCCACTGAACAACCTTCCCTACTCATGTCCTTAA 68

CC 61 ATGGGCAAACTTGCAGACG 82

CC 69 ATGGGCAAACTTGCAGACG 90

CC Db

CC AAV15382 standard; DNA; 90 BP.

CC AAV15382;

CC 20-JUL-1998 (first entry)

CC ApoE enhancer sense oligonucleotide.

CC Gene therapy; retrovirus; vector; apolipoprotein E; ApoE; enhancer;

CC human; interferon; ss.

CC Synthetic.

CC Homo sapiens.

CC WO9800542-A2.

CC 08-JAN-1998.

CC 02-JUL-1997; 97WO-US011785.

CC 03-JUL-1996; 96US-00645601.

CC 13-AUG-1996; 96US-00696381.

CC 04-JUN-1997; 97US-00869309.

CC (CHIR) CHIRON CORP.

XX (CHIR) CHIRON CORP.
 PA Jolly DJ, Barber JR, Chang SM, Respass JG, Allen JR, Boder M;
 PI Chong K, De la Vega D, Depolo NJ, Hsu DC, Ibanez CE;
 PI Mittelestaedt DM, Prussek CE, Greengard J;
 DR WPI, 1998-086967/08.
 XX New replication defective recombinant retroviruses - which express B
 PT domain-deleted human factor VIII or human factor IX for the treatment of
 PT haemophilia.
 PS Example 31; Page 144; 236pp; English.
 XX As apolipoprotein E (ApoE) enhancer cassette was generated from a set of
 CC 4 synthetic oligonucleotides (see AAV15382-85) that span the entire
 CC sequence. The oligonucleotides were phosphorylated at the 5' end. The
 CC first oligonucleotide (AAV15382) is the sense strand and contains a 5'
 CC HindIII site. The ApoE enhancer cassette was used, together with a liver-
 CC specific alpha-1-antitrypsin promoter, to control expression of
 CC interferon sequences in retroviral vectors. The invention relates to new
 CC recombinant gene delivery vehicles, such as replication-defective
 CC retroviral vectors, and their use in gene therapy of genetic diseases
 CC
 SQ Sequence 90 BP; 24 A; 25 C; 18 G; 23 T; 0 U; 0 Other;

Query Match 53.2%; Score 82; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACCTTACGCTACTCATGTCCTTAA 60
 DB 9 GTTTGTGCTGCTCTCTGAAGTCCACACTGAACAACCTTACGCTACTCATGTCCTTAA 68
 OY 61 ATGGGCAAAACATTCGACAGCAGC 82
 DB 69 ATGGGCAAAACATTCGACAGCAGC 90

RESULT 10
 AAV15386
 ID AAV15386 standard; DNA; 90 BP.
 AC AAV15386;
 XX 20-JUL-1998 (first entry)
 DT
 XX ApoE enhancer sense oligonucleotide.
 DE
 XX Interferon; human; gene therapy; retrovirus; vector; apolipoprotein E;
 KW ApoE; enhancer; ss.
 KW Synthetic.
 OS Homo sapiens.
 OS
 XX MO9800542-A2.
 PN
 XX 08-JAN-1998.
 PD
 XX 02-JUL-1997; 97WO-US011785.
 PP
 XX 03-JUL-1996; 96US-00645601.
 PR 13-AUG-1996; 96US-00656381.
 PR 04-JUN-1997; 97US-00869309.
 XX
 PA (CHIR) CHIRON CORP.
 PI Jolly DJ, Barber JR, Chang SM, Respass JG, Allen JR, Boder M;
 PI Chong K, De la Vega D, Depolo NJ, Hsu DC, Ibanez CE;
 PI Mittelestaedt DM, Prussek CE, Greengard J;
 DR WPI, 1998-086967/08.

XX New replication defective recombinant retroviruses - which express B
 PT domain-deleted human factor VIII or human factor IX for the treatment of
 PT haemophilia.
 PS Example 31; Page 146; 236pp; English.
 XX As apolipoprotein E (ApoE) enhancer cassette was generated from a set of
 CC 4 synthetic oligonucleotides (see AAV15386-89) that span the entire
 CC sequence. The oligonucleotides were phosphorylated at the 5' end. The
 CC first oligonucleotide (AAV15386) is the sense strand and contains a 5'
 CC EcoRI site. The ApoE enhancer cassette was used, together with a liver-
 CC specific alpha-1-antitrypsin promoter, to control expression of
 CC interferon sequences in retroviral vectors. The invention relates to new
 CC recombinant gene delivery vehicles, such as replication-defective
 CC retroviral vectors, and their use in gene therapy of genetic diseases
 CC
 SQ Sequence 90 BP; 25 A; 25 C; 17 G; 23 T; 0 U; 0 Other;

Query Match 53.2%; Score 82; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACCTTACGCTACTCATGTCCTTAA 60
 DB 9 GTTTGTGCTGCTCTCTGAAGTCCACACTGAACAACCTTACGCTACTCATGTCCTTAA 68
 OY 61 ATGGGCAAAACATTCGACAGCAGC 82
 DB 69 ATGGGCAAAACATTCGACAGCAGC 90

RESULT 11
 ADU47587
 ID ADU47587 standard; DNA; 90 BP.
 AC ADU47587;
 XX 27-JAN-2005 (first entry)
 DT
 XX Oligonucleotide #5 used to generate ApoE enhancer cassette.
 DE
 XX Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic;
 KW chymidine kinase; TK; ss; apolipoprotein E; Apo E.
 KW
 XX Unidentified.
 OS
 XX US6818439-B1.
 PN
 XX 16-NOV-2004.
 PD
 XX 30-DEC-1997; 97US-00001039.
 PP
 XX 30-DEC-1994; 94US-00367071.
 PR 03-JUL-1996; 96US-00645601.
 PR 13-AUG-1996; 96US-00656381.
 PR 04-JUN-1997; 97US-00869309.
 XX
 PA (CHIR) CHIRON CORP.
 PI Jolly DJ, Chang S, Respass JG, Depolo NJ, Hsu DC, Ibanez CE;
 PI Greengard J, Will L;
 PI WPI, 2004-793566/78.
 DR
 XX New high titre TK-1 retroviral vector expressing a factor VIII protein,
 PT useful in preparing a composition for treating hemophilia or thrombosis.
 PT
 PS Example 33; SEQ ID NO 65; 138pp; English.
 XX The present invention provides methods for obtaining measurable levels of
 CC a protein, nucleic acid molecule or enzymatic product in a bodily fluid
 CC or cells of a human. The method involves administering to a human a

recombinant retroviral preparation having a titer on HT1080 cells of greater than 10⁵ cfu/ml where the recombinant retroviral preparation is capable of directing the expression of a protein, nucleic acid molecule or enzyme which generates an enzymatic product such that measurable levels of the protein, nucleic acid molecule or enzymatic product may be obtained in the bodily fluid or cells of the human. The invention also relates to a novel TK (thymidine kinase)-1 retroviral vector which expresses a factor VIII protein. The TK-1 retroviral vector is useful in preparing a composition for treating haemophilia, thrombosis and other disorders. The invention is useful in gene therapy. The present sequence is an oligonucleotide used to generate apolipoprotein B (Apo B) enhancer cassette. This sequence is used in the method for administration of recombinant gene delivery vehicles for the treatment of haemophilia and other disorders.

Sequence 90 BP; 25 A; 25 C; 17 G; 23 T; 0 U; 0 Other;

Query Match 53.2%; Score 82; DB 13; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTGTGCTGCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCTTAA 60
DB 9 GTTGTGCTGCTCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCTTAA 68
OY 61 ATGGCAAAACATTGCAAGCAGC 82
DB 69 ATGGCAAAACATTGCAAGCAGC 90

RESULT 12

ADU47583
ADU47583 standard; DNA; 90 BP.

AC ADU47583;

DT 27-JAN-2005 (first entry)

XX Oligonucleotide #1 used to generate Apob enhancer cassette.

XX Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic;

XX thymidine kinase; TK; ss; apolipoprotein B; Apo B.

XX Unidentified.

XX US6818439-B1.

XX 16-NOV-2004.

XX 30-DEC-1997; 97US-00001039.

XX 30-DEC-1994; 94US-00367071.

XX 03-JUL-1996; 96US-00645601.

XX 13-AUG-1996; 96US-00696381.

XX 04-JUN-1997; 97US-00869309.

XX (CHIR) CHIRON CORP.

XX Jolly DJ, Chang S, Respass JG, Depolo NJ, Hsu DC, Ibanez CE;

XX Greengard J, Will L;

XX WPI; 2004-793566/78.

XX New high titer TK-1 retroviral vector expressing a factor VIII protein,

XX useful in preparing a composition for treating hemophilia or thrombosis.

XX Example 33; SEQ ID NO 61; 138bp; English.

XX The present invention provides methods for obtaining measurable levels of

XX a protein, nucleic acid molecule or enzymatic product in a bodily fluid

XX or cells of a human. The method involves administering to a human a

XX recombinant retroviral preparation having a titer on HT1080 cells of

XX greater than 10⁵ cfu/ml where the recombinant retroviral preparation is

capable of directing the expression of a protein, nucleic acid molecule or enzyme which generates an enzymatic product such that measurable levels of the protein, nucleic acid molecule or enzymatic product may be obtained in the bodily fluid or cells of the human. The invention also relates to a novel TK (thymidine kinase)-1 retroviral vector which expresses a factor VIII protein. The TK-1 retroviral vector is useful in preparing a composition for treating haemophilia, thrombosis and other disorders. The invention is useful in gene therapy. The present sequence is an oligonucleotide used to generate apolipoprotein B (Apo B) enhancer cassette. This sequence is used in the method for administration of recombinant gene delivery vehicles for the treatment of haemophilia and other disorders.

Sequence 90 BP; 24 A; 25 C; 18 G; 23 T; 0 U; 0 Other;

Query Match 53.2%; Score 82; DB 13; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTGTGCTGCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCTTAA 60
DB 9 GTTGTGCTGCTCTCTGAAGTCCACACTGAACAACCTTCACTCATGTCCTTAA 68
OY 61 ATGGCAAAACATTGCAAGCAGC 82
DB 69 ATGGCAAAACATTGCAAGCAGC 90

RESULT 13

AAV19599/C
AAV19599 standard; DNA; 82 BP.

AC AAV19599;

DT 25-MAR-2003 (revised)

DT 06-AUG-1998 (first entry)

XX Apolipoprotein B (Apo B) enhancer sequence generating antisense primer 3.

XX Replication defective; recombinant retrovirus; RRV; therapeutic protein;

XX haemophilia; thrombosis; hypercoagulable disorder; liver disease;

XX hepatitis; thalassemia; phenylketonuria; Leisch-Nyhan syndrome; human;

XX cystic fibrosis; Duchenne's muscular dystrophy; hypercholesterolemia;

XX diabetes; hypoparathyroidism; adenine deaminase deficiency; HIV infection;

XX anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;

XX autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein B; Apo B;

XX enhancer sequence; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9800541-A2.

XX 08-JAN-1998.

XX 02-JUL-1997; 97MO-US011784.

XX 03-JUL-1996; 96US-00645601.

XX 13-AUG-1996; 96US-00696381.

XX 04-JUN-1997; 97US-00869309.

XX (CHIR) CHIRON CORP.

XX Jolly DJ, Barber JR, Chang SM, Respass JG, Allen JR, Boder M;

XX Chong K, De La Vega D, Depolo NJ, Hsu DC, Ibanez CE;

XX Mittelestaedt DM, Prusaek CB, Greengard J, Lee R;

XX WPI; 1998-086966/08.

XX New replication defective recombinant retro-viruses - which can be

XX administered to provide long term systemic expression of therapeutic

XX protein in blood, useful in, e.g. treating hyper-coagulable disorders.

PS Example 33; Page 178; 272pp; English.

This primer is used for generating the apolipoprotein B (Apo B) enhancer sequence. This is used to construct a retroviral vector backbone with a liver specific promoter. The invention provides the preparation of a replication defective recombinant retrovirus (RRV) expressing a therapeutic protein. The RRV preparation is resistant to degradation by human complement and is capable of inducing long term systemic expression of the therapeutic protein when administered intravenously to a human. The long term systemic expression results in a measurable level of the therapeutic protein being produced in the blood of the human for a period of at least 30 days after the administration of the RRV vector preparation. The RRVs can be used for in vivo delivery of therapeutic protein to treat, e.g. haemophilia A, haemophilia B, thrombosis, hypercoagulable disorders, liver diseases such as hepatitis, disorders such as chalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe combined immunodeficiency (SCID), cystic fibrosis, Duchenne's muscular dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes, hypopituitarism, adenine deaminase deficiency, alpha-antitrypsin deficiency, Gaucher's syndrome, anaemia, infections such as HIV infection, high blood pressure, Alzheimer's disease, autoimmune or inflammatory disease or graft versus host disease. RRV's are capable of surviving inactivation in human serum thereby allowing efficient gene transfer over prolonged periods of time. (Updated on 25-MAR-2003 to correct PI field.)

SD Sequence 82 BP; 13 A; 21 C; 26 G; 22 T; 0 U; 0 Other;

Query Match	50.6%	Score 78:	DB 2:	Length 82;
Best Local Similarity	100.0%	Pred. No.	2.7e-15;	
Matches 78;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

DY 75 CAAGCAGCAACAGCAAACAACAGGCTCCCTGCCTGTGAACCTTGGAGCTGGGGGAGA 134
Dd 82 CAAACAGCAACAGCAAACAACAGGCTCCCTGCCTGTGAACCTTGGAGCTGGGGGAGA 23

QY 135 GGTCAAGAGACCTCTCTGG 152
|||
Db 22 GGTCAAGAGACCTCTCTGG 5

RESULT 14
ADU47589/c
ID ADU47589 standard; DNA; 82 BP.

AC ADU47589;

DT 27-JAN-2005 (first entry)

DE Oligonucleotide #7 used to generate ApoE enhancer cassette.

KM Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic
KM chymidine kinase; TK; ss; apolipoprotein E; Apo E.

OS Unidentified.

PN US6818439-B1.

PD 16-NOV-2004

30-DEC-1997; 97US-00001039.

PR 30-DEC-1994; 94US-00367071.

PR 13-AUG-1996; 96US-00696381.

XX
XX
XXXXX

2
1
1
1
2
4
2
2
1

PI Greengard J, Will

DR WPI; 2004-793566/78.

XX New high titre TK-1 retroviral vector expressing a factor VII protein,
PT useful in preparing a composition for treating hemophilia or thrombosis
PT
XX
XX
PS Example 33; SEQ ID NO 67; 138pp; English.

Example 33; SEQ ID NO 67; 138bp; English

CC The present invention provides methods for obtaining measurable levels of
CC a protein, nucleic acid molecule or enzymatic product in a bodily fluid
CC or cells of a human. The method involves administering to a human a
CC recombinant retroviral preparation having a titer on HT1080 cells of
CC greater than 10 5 cfu/ml where the recombinant retroviral preparation is
CC capable of directing the expression of a protein, nucleic acid molecule
CC or enzyme which generates an enzymatic product such that measurable
CC levels of the protein, nucleic acid molecule or enzymatic product may be
CC obtained in the bodily fluid or cells of the human. The invention also
CC relates to a novel TK (thymidine kinase)-1 retroviral vector which
CC expresses a factor VIII protein. The TK-1 retroviral vector is useful in
CC preparing a composition for treating haemophilia, thrombosis and other
CC disorders. The invention is useful in gene therapy. The present sequence
CC is an oligonucleotide used to generate apolipoprotein B (Apo B) enhancer
CC cassette. This sequence is used in the method for administration of
CC recombinant gene delivery vehicles for the treatment of haemophilia and
CC other disorders.

SQ Sequence 82 BP; 13 A; 21 C; 26 G; 22 T; 0 U; 0 Other;

Query Match	50.6%	Score 78:	DB 13:	length 82:
Best Local Similarity	100.0%	Pred. No.	2.7e-15:	
Matches 78:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0

Q7 75 CAAGCAGCAACAGCAACACAGCCCTCCCTGCTGTACCTTGGAGCTGGGGGACGA 134
Db 82 CAAGCAGCAACAGCAACACAGCCCTCCCTGCTGTACCTTGGAGCTGGGGGACGA 23

QY	135	GGTCAGAGACCTCTCTGG	152
Db	22	GGTCAGAGACCTCTCTGG	5

RESULT 15
AAV19595/c
ID AAV19595 standard; DNA; 82 BP

AC AAV19595;

DT 25-MAR-2003 (revised)

XX

[illegible]

KW haemophilia; thrombosis; hypercoagulable disorder; liver disease;
KW hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human

KW diabetes; hypertensive

KW autoimmune;

XX

OS Homo sapiens

PN WO9800541-A2

PD 08-JAN-1998.

PF 02-JUL-1997;

PR 03-JUL-1996;

PR 04-JUN-1997;

PA (CHIR) CHIR

XX Jolly DJ, Barber JR, Chang SMW, Respass JG, Allen JR, Boder M;
 PI Chong K, De la Vega D, Depolo NJ, Hsu DC, Ibanez CE;
 PI Mittelestedt DM, Prussak CB, Greengard J, Lee R;
 XX WPI: 1998-086966/08.

XX New replication defective recombinant retro-viruses - which can be
 PT administered to provide long term systemic expression of therapeutic
 PT protein in blood, useful in, e.g. treating hyper-coagulable disorders.

XX Example 33; Page 177; 272pp; English.

XX This primer is used for generating the apolipoprotein E (Apo E) enhancer
 CC sequence. This is used to construct a retroviral vector backbone with a
 CC liver specific promoter. The invention provides the preparation of
 CC replication defective recombinant retrovirus (RRV) expressing a
 CC therapeutic protein. The RRV preparation is resistant to degradation by
 CC human complement and is capable of inducing long term systemic expression
 CC of the therapeutic protein when administered intravenously to a human.
 CC The long term systemic expression results in a measurable level of the
 CC therapeutic protein being produced in the blood of the human for a period
 CC of at least 30 days after the administration of the RRV vector
 CC preparation. The RRV's can be used for in vivo delivery of therapeutic
 CC protein to treat, e.g. haemophilia A, haemophilia B, thrombosis,
 CC hypercoagulable disorders, liver diseases such as hepatitis, disorders
 CC such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe
 CC combined immunodeficiency (SCID), cystic fibrosis, Duchenne's muscular
 CC dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes,
 CC hypopituitarism, adenine deaminase deficiency, alpha1-antitrypsin
 CC deficiency, Gaucher's syndrome, anaemia, infections such as HIV
 CC infection, high blood pressure, Alzheimer's disease, autoimmune or
 CC inflammatory disease or graft versus host disease. RRV's are capable of
 CC surviving inactivation in human serum thereby allowing efficient gene
 CC transfer over prolonged periods of time. (Updated on 25-MAR-2003 to
 CC correct PI field.)

XX SQ Sequence 82 BP; 12 A; 21 C; 27 G; 22 T; 0 U; 0 Other;

Query Match 50.0%; Score 77; DB: 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 5.8e-15;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 CAAGCAGCAACAGCAACACAGAGCCCTCCCTGCTGACCTTGAGAGCTGGGCGAGA 134
 DB 82 CAAGCAGCAACAGCAACACAGAGCCCTCCCTGCTGACCTTGAGAGCTGGGCGAGA 23
 OY 135 GGTGAGAGACCTCTCTG 151
 DB 22 GGTGAGAGACCTCTCTG 6

Search completed: April 18, 2006, 13:22:04
 Job time : 95.4261 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: April 18, 2006, 12:18:29 ; Search time 747.823 Seconds
(without alignments)
9634.919 Million cell updates/sec

Title: US-09-884-901a-8

Perfect score: 154
Sequence: 1 gttctgtgtcgtcctctgaa.....gttcagagacctctctgagc 154

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: gb-est1.*
2: gb-est2.*
3: gb-est3.*
4: gb-hlc.*
5: gb-est4.*
6: gb-est5.*
7: gb-est6.*
8: gb-est7.*
9: gb-g881.*
10: gb-g882.*
11: gb-g883.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	38	24.7	958	10	CNS0044W
C 2	36.2	23.5	329	6	CB458659 717364 MA
C 3	35.6	23.1	643	1	AU279008 AU279008
C 4	35.4	23.0	469	8	CK307208 C19002006
C 5	35.2	22.9	363	7	CK779717
C 6	35.2	22.9	401	7	CK727732 UMC-bend
C 7	35.2	22.9	479	2	BF042501 BP250012A
C 8	35.2	22.9	567	1	AU279081 AU279081
C 9	35.2	22.9	579	2	BF043702 BP250015B
C 10	35.2	22.9	615	6	CB434484 611104 MA
C 11	35.2	22.9	716	6	CB457803 715917 MA
C 12	35.2	22.9	732	7	CK970120 4085432 B
C 13	35.2	22.9	742	7	CK970120 4085470 B
C 14	35.2	22.9	825	8	DN526096 1270831 M
C 15	35.2	22.9	941	8	DN523404 1266895 M
C 16	35	22.7	554	2	AO992245 nbep00851
C 17	35	22.7	735	2	BE263325 601190812
C 18	35	22.7	1014	2	BG751214 602730325
C 19	34.2	22.2	792	11	CR806205 GROMAA28A
C 20	34	22.1	289	9	AZ096407 RPCI-23-4
C 21	33.8	21.9	737	10	AG406290 Mus muscu
C 22	33.8	21.9	1346	2	BG495013 602541679

C 23	33.6	21.8	311	6	CB696796
C 24	33.6	21.8	335	1	AM631727
C 25	33.6	21.8	432	8	R48041
C 26	33.6	21.8	838	5	BW326878
C 27	33.6	21.8	972	5	BW356799
C 28	33.4	21.7	430	2	BP501783
C 29	33.4	21.7	528	2	BP498419
C 30	33.4	21.7	549	2	BE978332
C 31	33.4	21.7	617	10	CL719165
C 32	33.4	21.7	639	10	CL746108
C 33	33.4	21.7	667	10	CL770284
C 34	33.4	21.7	764	10	CL712133
C 35	33.4	21.7	835	10	CL726784
C 36	33.4	21.7	835	10	CL965232
C 37	32.8	21.3	444	5	BY388939
C 38	32.8	21.3	477	9	AZ787078
C 39	32.8	21.3	554	3	BW547747
C 40	32.8	21.3	583	10	AG973280
C 41	32.8	21.3	623	10	AG970743
C 42	32.8	21.0	1049	3	BM423372
C 43	32.4	21.0	467	3	BP614956
C 44	32.4	21.0	640	9	CE010717
C 45	32.4	21.0	752	7	CP951791

ALIGNMENTS

RESULT 1
CNS0044W/C
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR09M23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
AL066467
AL066467.1 GI:4942910
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
ORGANISM
Bukariyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITL
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)

COMMENT
- Web : www.genoscope.cns.fr
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mamoser in Peter de Jong's laboratory in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1..958
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR09M23"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

Query Match	24.7%	Score 38	DB 10	Length 958
Best Local Similarity	38.9%	Pred. No. 2		
Matches	49	Conservative	29	Mismatches 48; Indels 0; Gaps 0
Db	2	TTGTGTGCTGCTCTGAAGTCCACATGCAACAACTTCAGCTACTACTATGTCCTTAAAA	61	
Qy	684	TTTTTTTTTATTTTTCGTCGGCGAMMAAAACMAATTTTTCGTCGAMCAGTCCCAAAT	625	
Db	62	TGGGCAACATGCAAGCAAGCAACAAACACACAGCCCTCCCTGCTGTGACCTTG	121	
Qy	624	TGSCCAASGKCCCAATTTTMAAAATHTTMAAAAMMMKXVDSGCCAGCTTCTT	565	
Db	122	GAGCTG	127	
Qy	564	GAGMTG	559	
RESULT 2				
LOCUS	CB458659	329 bp	mRNA	linear
DEFINITION	717364 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.			
ACCESSION	CB458659			
VERSION	CB458659.1	GI:29265043		
KEYWORDS	EST.			
SOURCE	Bos taurus (cow)			
ORGANISM	Bos taurus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
AUTHORS	1 (bases 1 to 329) Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keefe,J.W.			
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov			
FEATURES	Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: FQY8072 row: D column: 12 Seq primer: TAGAGGCACTGCGAGG.			
source	Location/Qualifiers 1..329 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_id="MARC 6BOV" /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."			
ORIGIN				
Query Match	23.5%	Score 36.2	DB 6	Length 329
Best Local Similarity	59.0%	Pred. No. 5.5		
Matches	62	Conservative	0	Mismatches 43; Indels 0; Gaps 0
Db	11	TGCTCTGAATCCACACTGAACAACTTCAGCTACTGATGCTTAAATGGGCAAC	70	
Qy	112	TGCCAGAAATTAATAAATAAGCAACTTCAGCTCCCACTTCCAACTATACGAAC	53	
Db	71	ATTGCAAGCAGCAACACAGCAACACACAGCCCTCCCTGCTGCTG	115	
Qy	52	AATTTATTCAGAGTGAAAAAACAAGTAAGAACCTGTCTGCTG	8	

LOCUS	AU279008	643 bp	mRNA	linear	EST 02-JUL-2002
DEFINITION	AU279008 Cloned bovine placenta cDNA Bos taurus cDNA clone Placentai36 3', mRNA sequence.				
ACCESSION	AU279008				
VERSION	AU279008.1	GI:21682318			
KEYWORDS	EST.				
SOURCE	Bos taurus (cow)				
ORGANISM	Bos taurus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.				
AUTHORS	Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and Sasaki,Y.				
TITLE	EST analysis of cloned bovine fetus and placenta				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Masahito Oishi Graduate School of Agriculture Kyoto University Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan Tel.: 81-75-753-6331 Fax: 81-75-753-6340 Email: oishi@kans.jkans.kais.kyoto-u.ac.jp. Location/Oallifiers				
FEATURES	1..643				
SOURCE	/organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /clone="placentai366" /dev_stage="60 embryonic day" /clone_1ib="Cloned bovine placenta cDNA"				
ORIGIN					
Query Match	23.1%; Score 35.6; DB 1; Length 643;				
Best Local Similarity	58.5%; Pred. No. 9.7;				
Matches	62; Conservative 0; Mismatches 44; Indels 0; Gaps 0;				
DY	11 TGCCTGAGTCCACACTGAACAACCTTCAGCTCACTCATGTCCCTTAATAATGGCAAC 70				
Db	176 TGCCAGAAATTAAAAAATAAGAACCTTCAGCTCCCCCANTCTCAACAAATACAGAACC 117				
DY	71 ATTGAAGCGCAACAGCAACACACAGCCCTCCCTGCCCTGCTGA 116				
Db	116 AATTATTTCAGAGTGAAAANAACGTAAAGAACTGTCTGCTTA 71				
RESULT 4					
CX307208	469 bp	mRNA	linear	EST 06-MAY-2005	
LOCUS	C19002D6E77 PlayFrSubl Citrus clementina x Citrus tangerina cDNA				
DEFINITION	Clone C19002D06, mRNA sequence.				
ACCESSION	CX307208				
VERSION	CX307208.1	GI:63076062			
KEYWORDS	EST.				
SOURCE	Citrus clementina x Citrus tangerina				
ORGANISM	Citrus clementina x Citrus tangerina				
REFERENCE	Bakayrote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.				
AUTHORS	1 (bases 1 to 469) Formet J., Gadea,J., Huerta,L., Abizanda,L., Agusti,J., Almar,S., Alós,B., Andres,F., Arribas,R., Beltran,J.P., Berbel,A., Blazquez,M.A., Brumos,J., Canas,L.A., Cercos,M., Colmenero-Piñeres,J.M., Coneas,A., Estabbes,B., Gandía,M., Garcla-Martinez,J.J., Gimeno,J., Gisbert,A., Gomez,G., Gonzalez-Candelas,L., Granell,A., Guert,J., Latuene,M.T., Medueno,F., Marcos,J.F., Marques,M.C., Martinez,P., Martinez-Godoy,M.A., Miralles,S., Moreno,P., Navarro,I., Pallas,V., Perez-Amador,M.A., Perez-Valle,J., Pons,C., Rodrigo,I., Rodriguez,P.L., Royo,C., Serrano,R., Soler,G., Tadeo,F., Talon,M., Terol,J., Trenor,M., Vaello,L., Vicente,O., Vidal,Ch., Zacarias,L. and Conejero,V.				

TITLE Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies
JOURNAL Plant Mol. Biol. 57 (3), 375-391 (2005)
PUBMED 15830128
COMMENT Contact: Forment J
 Genomics Laboratory
 Instituto de Biología Molecular y Celular de Plantas (Universidad Politécnica de Valencia - Consejo Superior de Investigaciones Científicas)
 Avenida de los Naranjos s/n, 46022 Valencia, Spain
 Email: jforment@lmcpc.upv.es

FEATURES
source
 1..469
 /organism="Citrus clementina x Citrus tangerina"
 /mol_type="mRNA"
 /cultivar="Fortune"
 /db_xref="taxon:307631"
 /clone="C19002D06"
 /sex="hermaphrodite"
 /tissue_type="flavado"
 /dev_stage="adult trees"
 /lab_host="Escherichia coli"
 /clone_lib="PlavF-Sub1"
 /note="Organ: fruits; Vector: PCR2.1; Subtracted cDNA library made from poly-A+ RNA from flavado of fruits stored at 20C for 14 days, subtracted with poly-A+ RNA from fruits stored at 120C for 14 days"

ORIGIN
 Query Match 23.0%; Score 35.4; DB 8; Length 469;
 Best Local Similarity 55.2%; Pred. No. 10;
 Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 29 TGAACAACTTACGCTACTCATGTCCCTAAATGGCAACATTGCAAGCAGCAAG 88
 |||
 248 TGTATTCATTTGGCGGTATACACTGTCCAAATATGAAGAAGCAGCAGCAAAACA 307
 |||

QY 89 CAACACAGACGCTCTCTGCTGTGACCTTGAAGCTGGGCGAGAGCTCAGACCTCT 148
 |||

Db 308 TGAAGCAGCAGCTAACACTGCTTCAAGGCGCGGCTGCGCCAAATATCTGGAACCTTC 367
 |||

QY 149 CTGGG 153
 |||

Db 368 CAGAG 372
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RESULT 5
LOCUS CK779717 363 bp mRNA linear EST 23-PEB-2004
DEFINITION UMC-bend_0B01-012-g01 Day 8 Uterus bend Bos taurus cDNA 3', mRNA
 sequence.
ACCESSION CK779717
VERSION CK779717.1 GI:42745395
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 363)
 Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C.,
 Roberts, R.M., Smith, M.F. and Youngquist, R.S.
 USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
 Reproduction
 Unpublished (2002)
REFERENCE Contact: DNA Core Facility (Bovine Project)
 Animal Science - RS Prather
 University of Missouri-Columbia
 M616 Medical Sciences Bldg., Columbia, MO 65212, USA
 Tel: (573) 882-0428
 Fax: (573) 884-5552
 Email: bovine@net.missouri.edu
AUTHORS POLYA=Yes.

FEATURES
source

Location/Qualifiers
 1..363
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone_lib="bend"

/note="Funding: The production of ESTs submitted in this project was funded by USDA Grant NRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather, E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Sources: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlea-ranch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL:
<http://genome.net.missouri.edu/Bovine/Methods.html>.
library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAR-60 reagent (Tel-Test, Friendwood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at 637 degrees with 10mcg of NotI-tag-dt18 oligonucleotide. (GCTGCTGGCGCCG-tag-T18) and reverse transcribed at 637 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/softwre.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dt18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were

Location/Qualifiers
1. .401 .

TAG_SSD=CTGACACTTG"

JOURNAL COMMENT
Unpublished (2002)
Contact: DNA Core Facility (Bovine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA

(3) 882-0428
(3) 884-5552
bovine@net.missouri.edu

Location/Qualifiers
1. 401
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone_1lb="Bend"

/note="Funding: The production of ESTs submitted in this project was funded by USDA Grant WRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather, B Antonini, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Helpers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These helpers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL:
<http://genome.net.missouri.edu/Bovine/Methods.html>.
Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Scarsz et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using TRIzol-60 reagent (TRI-Less, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by R. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the Superscript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-dfr18 oligonucleotide (GCTGTCCGGCGC-tag-T18) and reverse transcribed at c37 degrees with Superscript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a deoxyriphatase (Tiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.nwca.edu/pubsoft/scsoftware.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adaptors (Invitrogen-life technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A+ RNA was isolated by using the MicroPilot(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dfr18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence

complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with plu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary library characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group (Spollen WG, Topinka CW, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core Facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res. 1996; 6:791-806. Jiang H, Bivens NJ, Ries JB, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Matchalagan N, Pletcher RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MR Bonaldo, P Jeleno, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci. 91:9228-9232. TAG_Seq=not found"

ORIGIN

Query Match 22.9%; Score 35.2; DB 7; Length 401;
Best Local Similarity 58.7%; Pred. No. 12;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 11 TGCCTGAGTCCACACTGAAACAATCTGACCTACTGATGCTCTAAATGGGCAAC 70
DB 112 TGGCCAGAAATTAATAAATAAGCACTTCCAGCCCTCCATCTCCACAAATACGAAAC 171
QY 71 ATTGCAAGCAGCAACAGCAACACACAGCCCTCCCTGCTGCT 114
DB 172 AATTATTTCAGAAAGTGAATAAAGCAAGTAAAGAACTGTCTGCT 215

RESULT 7
LOCUS BP042501 479 bp mRNA linear EST 10-OCT-2000
DEFINITION BP250012A10B5 Soares normalized bovine placenta Bos taurus cDNA
clone BP250012A10B5 5', mRNA sequence.
ACCESSION BP042501
VERSION BP042501.1 GI:10759556
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 479)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
Latson,J.H.
Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi G:
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTACCTCCTAATG
Insert Length: 479 Std Error: 0.00
Plate: BP250012A10 Row: B Column: 5
Seq primer: AGCGATACCAATTCACACGGA
High quality sequence stop: 479.
Location/Qualifiers
1..479
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BP250012A10B5"
/sex="female"
/lab_host="DH10B"
/clone_lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pTZ19; Site 1: Scott;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

FEATURES

SOURCE

ORIGIN

Query Match 22.9%; Score 35.2; DB 2; Length 479;
Best Local Similarity 58.7%; Pred. No. 12;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 11 TGCCTGAGTCCACACTGAAACAATCTGACCTACTGATGCTCTAAATGGGCAAC 70
DB 127 TGGCCAGAAATTAATAAATAAGCACTTCCAGCCCTCCATCTCCACAAATACGAAAC 186
QY 71 ATTGCAAGCAGCAACAGCAACACACAGCCCTCCCTGCTGCT 114
DB 187 AATTATTTCAGAAAGTGAATAAAGCAAGTAAAGAACTGTCTGCT 230

RESULT 8
LOCUS AU279081 567 bp mRNA linear EST 02-JUL-2002
DEFINITION AU279081 Cloned bovine placenta cDNA Bos taurus cDNA clone
Placental1520 3', mRNA sequence.
ACCESSION AU279081
VERSION AU279081.1 GI:21682391
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
Oishi,M., Yamada,T., Goma,H., Iejukole,H.Y., Taniguchi,Y. and
Sasaki,Y.
EST analysis of cloned bovine fetus and placenta
Unpublished (2002)
Contact: Masahito Oishi
Graduate School of Agriculture
Kyoto University
Sakyo-Kitaashirakawa, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-6331
Fax: 81-75-753-6340
Email: oishi@kans.jkans.kais.kyoto-u.ac.jp.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
SOURCE

Location/Qualifiers
1..567
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="placenta1520"
/dev_stage="60 embryonic day"
/clone_1ib="Cloned bovine placenta cdna"

ORIGIN

Query Match 22.9%; Score 35.2; DB 1; Length 567;
Best Local Similarity 58.7%; Pred. No. 12;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

11 TGCCCTGAGTCCACCTGCAACAACTTCAGCTCTACATGTCCTTAATGGGCAAC 70
105 TGCCAGAGATTAAATAATTAAGCACTTCAGCTCTCCCACTTCAACAATACAGAAC 46

71 ATTGCAAGCAGCAACAGCAACACAGACCCCTCCCTGCT 114
45 AATTATTTCAGAGTGAATAAAGAGTAAGAACCTGTCTGCT 2

RESULT 9 579 bp mRNA linear EST 10-OCT-2000
LOCUS BP250015B10E12 Soares normalized bovine placenta Bos taurus cdna.
DEFINITION BP250015B10E12 5', mRNA sequence.
ACCESSION BP043702
VERSION BP043702.1 GI:10760757
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 579)
AUTHORS Lewin,H.A., Soares,M.B., Rebelz,M., Pardinas,J., Liu,L. and
Larsen,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-6534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross-match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACCTCCTAATAG
Insert length: 579 Std Error: 0.00
Plate: BP250015B10 row: E column: 12
Seq primer: AGCGATACATTTCAACAGCA
High quality sequence stop: 579.

FEATURES
SOURCE

Location/Qualifiers
1..579
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BP250015B10E12"
/sex="female"
/lab_host="DH10B"
/clone_1ib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pTZ193a; Site 1: EcoRI;
Site 2: NotI; The cdna library was contributed by the

ORIGIN

Query Match 22.9%; Score 35.2; DB 2; Length 579;
Best Local Similarity 58.7%; Pred. No. 13;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

11 TGCCCTGAGTCCACCTGCAACAACTTCAGCTCTACATGTCCTTAATGGGCAAC 70
136 TGCCAGAGATTAAATAATTAAGCACTTCAGCTCTCCCACTTCAACAATACAGAAC 195

71 ATTGCAAGCAGCAACAGCAACACAGACCCCTCCCTGCT 114
196 AATTATTTCAGAGTGAATAAAGAGTAAGAACCTGTCTGCT 239

RESULT 10 615 bp mRNA linear EST 25-MAR-2003
LOCUS CB434484
DEFINITION 61104 MARC 6BOV Bos taurus cdna 5', mRNA sequence.
ACCESSION CB434484
VERSION CB434484.1 GI:29214562
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 615)
AUTHORS Smith,T.P.L., Roberts,A.J., Echeverkamp,S.E., Chitko-McKown,C.G.,
Wray,J.B. and Keel,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alc option. Vector identified with
cross_match v0.990329.
Plate: FQY8034 row: P column: 15
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
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FEATURES
SOURCE

/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 22.9%; Score 35.2; DB 6; Length 615;
Best Local Similarity 58.7%; Pred. No. 13;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

11 TGCCCTGAGTCCACCTGCAACAACTTCAGCTCTACATGTCCTTAATGGGCAAC 70
335 TGCCAGAGATTAAATAATTAAGCACTTCAGCTCTCCCACTTCAACAATACAGAAC 394

71 ATTGCAAGCAGCAACAGCAACACAGACCCCTCCCTGCT 114
395 AATTATTTCAGAGTGAATAAAGAGTAAGAACCTGTCTGCT 438

RESULT 11
CB457803 716 bp mRNA linear EST 26-MAR-2003
LOCUS 715917 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION CB457803
ACCESSION CB457803.1 GI:29264185
VERSION EST.
KEYWORDS Bos taurus (cow)
SOURCE
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 716)
Smith, T.P.L., Roberts, A.J., Botherkamp, S.R., Chitko-McKown, C.G., Wray, J.E. and Keeler, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@meat.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim.alt option. Vector identified with cross_match v0.990329.
Plate: FQ78073 row: C column: 5
Seq primer: GTAATACGATCCTCATCTATGAGG.
location/Qualifiers
1..716
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."

ORIGIN
Query Match 22.9%; Score 35.2; DB 6; Length 716;
Best Local Similarity 58.7%; Pred. No. 13; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 43

QY 11 TGCCCTGAGTCACACCTGAAACAACTTCACTCATGTCCCTAAATGGCAAC 70
DB 77 TCCCGAGATTTAAATAATTAAGCACTTCACTCCCATCTCCAAATAATACAGAAC 136
QY 71 ATTGCAGACGAAACAGCAACACACAGCCCTCCCTGCTCT 114
DB 137 AATTATTCAGAGTGAATAAAACAGTAAAGAACTGTCTGCT 180

RESULT 12
CK970120 732 bp mRNA linear EST 16-MAR-2004
LOCUS 4085432 BARC 9BOV Bos taurus cDNA clone 9BOV2_A09 5', mRNA
DEFINITION CK970120
ACCESSION CK970120.1 GI:45488094
VERSION EST.
KEYWORDS Bos taurus (cow)
SOURCE
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 732)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassel, C.P., Harhay, G.P., Bosak, S., Rubenstein, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut

JOURNAL
COMMENT Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.000925 using options "-trim alt" -trim fasta. Vector identified by cross_match using options "-mismatch 12 -mismatch 12 Plate: 2 row: A column: 09
Seq primer: CCCAGTCACGACGTGTAAACG
High quality sequence stop: 732.
location/Qualifiers
1..732
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV2_A09"
/sex="Male"
/tissue_type="pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pXen-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of 18 and 21 week old steers. fundic and pyloric abomasus of 18 and 21 week old steers. Exposure to Oerteragia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"

ORIGIN
Query Match 22.9%; Score 35.2; DB 7; Length 732;
Best Local Similarity 58.7%; Pred. No. 13; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 43

QY 11 TGCCCTGAGTCACACCTGAAACAACTTCACTCATGTCCCTAAATGGCAAC 70
DB 87 TCCCGAGATTTAAATAATTAAGCACTTCACTCCCATCTCCAAATAATACAGAAC 146
QY 71 ATTGCAGACGAAACAGCAACACACAGCCCTCCCTGCTCT 114
DB 147 AATTATTCAGAGTGAATAAAACAGTAAAGAACTGTCTGCT 190

RESULT 13
CK834244 742 bp mRNA linear EST 04-MAR-2004
LOCUS 4058470 BARC 8BOV Bos taurus cDNA clone 8BOV_2D12 5', mRNA
DEFINITION CK834244
ACCESSION CK834244.1 GI:45064530
VERSION EST.
KEYWORDS Bos taurus (cow)
SOURCE
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 742)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassel, C.P. and Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated from Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
Bldg 162: BARC-East, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt '-trim fasta. Vector identified by cross match using options -mismatch 12 -mismatch 12

Seq primer: CCTATTAGTGACCTATAGAC
High quality sequence stop: 742.

FEATURES

source

1. 742
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV 2D12"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TON3"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1: NotI; Site 2: EcoRI; Normalized cow cDNA intestinal library in pCMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating, proximal duodenum, 1 neonatal intestinal 4/5 lactating, proximal duodenum, 1 jejunal, distal ileum, colon, 1/5 neonatal, proximal duodenum, jejunal, distal ileum"

ORIGIN

Query Match 22.9%; Score 35.2; DB 7; Length 742;
Best Local Similarity 58.7%; Pred. No. 13; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

11 TGCCCTGAGTCCACCTGAAACAACTTCAGCTCTCATGTCCTTAATGGGCAAC 70
Db 599 TGCCAGGAAATTAATAAATAGCACTTCAGCTCCCACTCCCAACAAATACGAAAC 658
71 ATTGCAAGCAGCAACGCAACACACACGCTCCCTGCTGCT 114
Db 659 AATTATTGAGAGTGAAGAAAAACGTAAGGAACTGTCTGCT 702

RESULT 14

LOCUS DMS26096 825 bp mRNA linear EST 11-MAR-2005
DEFINITION 1270831 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION DMS26096
VERSION DMS26096.1 GI:60971328
KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keefe,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: RUK8044 row: A column: 11
Seq primer: GTAATACGACTCTATAGG.
Location/Qualifiers

FEATURES

source

1. 825
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"

ORIGIN

/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

Query Match 22.9%; Score 35.2; DB 8; Length 825;
Best Local Similarity 58.7%; Pred. No. 14; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

11 TGCCCTGAGTCCACCTGAAACAACTTCAGCTCTCATGTCCTTAATGGGCAAC 70
Db 205 TGCCAGGAAATTAATAAATAGCACTTCAGCTCCCACTCCCAACAAATACGAAAC 264
71 ATTGCAAGCAGCAACGCAACACACACGCTCCCTGCTGCT 114
Db 265 AATTATTGAGAGTGAAGAAAAACGTAAGGAACTGTCTGCT 308

RESULT 15

LOCUS DMS23404 941 bp mRNA linear EST 11-MAR-2005
DEFINITION 1266895 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION DMS23404
VERSION DMS23404.1 GI:60966258
KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keefe,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: RUK8044 row: A column: 11
Seq primer: TAGAAGCAGACGTGAGG.
Location/Qualifiers

FEATURES

source

1. 941
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

ORIGIN

Query Match 22.9%; Score 35.2; DB 8; Length 941;
Best Local Similarity 58.7%; Pred. No. 14; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

11 TGCCCTGAGTCCACCTGAAACAACTTCAGCTCTCATGTCCTTAATGGGCAAC 70
Db 803 TGCCAGGAAATTAATAAATAGCACTTCAGCTCCCACTCCCAACAAATACGAAAC 744
71 ATTGCAAGCAGCAACGCAACACACACGCTCCCTGCTGCT 114

Db 743 AATTATTGAGAGTGAAAAACAGTAAGGAACCTGTCTGCT 700

Search completed: April 18, 2006, 15:20:35
Job time : 751.823 secs

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: GENERAL INFORMATION:
: APPLICANT: Miao, Carol
: APPLICANT: Kay, Mark
: TITLE OR INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use

```

FILE REFERENCE: U0FM-1-17396
CURRENT APPLICATION NUMBER: US/09/884,901
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/212,902
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 328
TYPE: DNA
ORGANISM: Homo Sapien
US-09-884-901-9

Query Match 100.0%; Score 154; DB 3; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.5e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 60
DB 78 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 137
QY 61 ATGGGCAAACTTGCAGACGCAACAAACAGCAAGCCCTCTGCTGCTGACCTT 120
DB 138 ATGGGCAAACTTGCAGACGCAACAAACAGCAAGCCCTCTGCTGCTGACCTT 197
QY 121 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 154
DB 198 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 231

RESULT 3

US-09-884-901-4
Sequence 4, Application US/09884901
Patent No. US20020076798A1
GENERAL INFORMATION:
APPLICANT: Mayo, Mark
TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
FILE REFERENCE: U0FM-1-17396
CURRENT APPLICATION NUMBER: US/09/884,901
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/212,902
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 771
TYPE: DNA
ORGANISM: Homo Sapien
US-09-884-901-4

Query Match 100.0%; Score 154; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 3.2e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 60
DB 78 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 137
QY 61 ATGGGCAAACTTGCAGACGCAACAAACAGCAAGCCCTCTGCTGCTGACCTT 120
DB 138 ATGGGCAAACTTGCAGACGCAACAAACAGCAAGCCCTCTGCTGCTGACCTT 197
QY 121 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 154
DB 198 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 231

RESULT 4

US-09-863-733A-100
Sequence 100, Application US/09863733A
Publication No. US20030082537A1
GENERAL INFORMATION:

APPLICANT: Stanton, Jr., Vincent P.
TITLE OF INVENTION: METHODS FOR GENETIC ANALYSIS OF DNA
FILE REFERENCE: 11926-113001
CURRENT APPLICATION NUMBER: US/09/863,733A
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/697,028
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: 09/696,998
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: 09/697,013
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: 60/206,613
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 100
LENGTH: 10527
TYPE: DNA
ORGANISM: Homo sapiens
US-09-863-733A-100

Query Match 100.0%; Score 154; DB 3; Length 10527;
Best Local Similarity 100.0%; Pred. No. 7e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 60
DB 9668 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 9727
QY 61 ATGGGCAAACTTGCAGACGCAACAAACAGCAAGCCCTCTGCTGCTGACCTT 120
DB 9728 ATGGGCAAACTTGCAGACGCAACAAACAGCAAGCCCTCTGCTGCTGACCTT 9787
QY 121 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 154
DB 9788 GGAGCTGGGGCAGAGGTCAAGACCTCTCTGGGC 9821

RESULT 5

US-10-116-420-100
Sequence 100, Application US/10116420
Publication No. US20030073101A1
GENERAL INFORMATION:
APPLICANT: Stanton, Jr., Vincent P.
APPLICANT: Olson, Jeffrey
TITLE OF INVENTION: RESTRICTION ENZYME GENOTYPING
FILE REFERENCE: 11926-167001
CURRENT APPLICATION NUMBER: US/10/116,420
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 09/863,733
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/697,028
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 09/696,998
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 09/697,013
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 60/206,613
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 100
LENGTH: 10527
TYPE: DNA
ORGANISM: Homo sapiens
US-10-116-420-100

Query Match 100.0%; Score 154; DB 5; Length 10527;
Best Local Similarity 100.0%; Pred. No. 7e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTGTGCTGCTCTGAAGTCCACACTGAACAACTTCAAGCCTACTCATGTCCCTAAA 60

Db 9668 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAAGCTTCAATGCTCTTAA 9727
Qy 61 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 120
Db 9728 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 9787
Qy 121 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 154
Db 9788 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 9821

RESULT 6
US-10-287-964-95
; Sequence 95, Application US/10287964
; Publication No. US20030219769A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Jeffrey
; APPLICANT: Zillmann, Martin
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: METHODS FOR GENETIC ANALYSIS OF DNA USING BIASED AMPLIFICATION OF
; TITLE OF INVENTION: POLYMORPHIC SITES
; FILE REFERENCE: 11926-016002
; CURRENT APPLICATION NUMBER: US/10/287, 964
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/696, 998
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/206, 613
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 10527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-964-95

Query Match 100.0%; Score 154; DB 6; Length 10527;
Best Local Similarity 100.0%; Pred. No. 7e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAAGCTTCAATGCTCTTAA 60
Db 9668 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAATGCTCTTAA 9727
Qy 61 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 120
Db 9728 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 9787
Qy 121 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 154
Db 9788 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 9821

RESULT 7
US-10-741-601-5756
; Sequence 5756, Application US/10741601
; Publication No. US2004016519A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741, 601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5756
; LENGTH: 16963
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-5756

Query Match 100.0%; Score 154; DB 7; Length 16963;
Best Local Similarity 100.0%; Pred. No. 8e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAAGCTTCAATGCTCTTAA 60
Db 15958 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAAGCTTCAATGCTCTTAA 16017
Qy 61 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 120
Db 16018 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 16077
Qy 121 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 154
Db 16078 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 16111

RESULT 8
US-10-741-600-17945
; Sequence 17945, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741, 600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17945
; LENGTH: 16963
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17945

Query Match 100.0%; Score 154; DB 8; Length 16963;
Best Local Similarity 100.0%; Pred. No. 8e-43;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAAGCTTCAATGCTCTTAA 60
Db 15958 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACCTTCAATGCTCTTAA 16017
Qy 61 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 120
Db 16018 ATGGGCAAACTTGCAGACGAAACAGCAAGAGCCCTCTGCTGCTGACTT 16077
Qy 121 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 154
Db 16078 GGAGCTGGGGCAGAGGTCAAGAGACTTCTTGGGC 16111

RESULT 9
US-09-967-013-5
; Sequence 5, Application US/09967013
; Patent No. US20020045840A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 11926-022001
; CURRENT APPLICATION NUMBER: US/09/967, 013
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 60/206, 613
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 41907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-013-5

Query Match 100.0%; Score 154; DB 3; Length 41907;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAA 60
DB 36908 GTTGTGTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAA 36967
QY 61 ATGGGCAAACTTGCAGACGAAACAGAAACACAGCCCTCTGCTGACCTT 120
DB 36968 ATGGGCAAACTTGCAGACGAAACAGAAACACAGCCCTCTGCTGACCTT 37027
QY 121 GGAGCTGGGGGAGAGGTGAGAGACCTCTGAGGC 154
DB 37028 GGAGCTGGGGGAGAGGTGAGAGACCTCTGAGGC 37061

RESULT 10

US-10-100-235-11
Sequence 11, Application US/10100235
Publication No. US20030147853A1
GENERAL INFORMATION:
APPLICANT: MCCLELLAND, Alan
APPLICANT: SCOLLAY, Roland
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS-MEDIATED GENE
FILE REFERENCE: 0800-0027
CURRENT APPLICATION NUMBER: US/10/100.235
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 60/275,908
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Apob HCR
US-10-100-235-11

Query Match 98.1%; Score 151; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-42;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAA 60
DB 4 GTTGTGTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAA 63
QY 61 ATGGGCAAACTTGCAGACGAAACAGAAACACAGCCCTCTGCTGACCTT 120
DB 64 ATGGGCAAACTTGCAGACGAAACAGAAACACAGCCCTCTGCTGACCTT 123
QY 121 GGAGCTGGGGGAGAGGTGAGAGACCTCTGAGGC 151
DB 124 GGAGCTGGGGGAGAGGTGAGAGACCTCTGAGGC 154

RESULT 11

US-10-972-50807/c
Sequence 50807, Application US/10972079
Publication No. US2005015317A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: KERR, Richard
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEE
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: NM1110-2

CURRENT APPLICATION NUMBER: US/10/972.079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50807
LENGTH: 568
TYPE: DNA
ORGANISM: Chicken
US-10-972-50807

Query Match 23.6%; Score 36.4; DB 9; Length 568;
Best Local Similarity 56.8%; Pred. No. 0.037;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 7 GTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAAATGGGC 66
DB 465 GTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAAATGGGC 406
QY 67 AAACATTGCAAGCAGCAAAACAGCAACACAGCCCTCTGCTGACCTTGGAG 124
DB 405 GCACTGCGCAGCAGCGCATCTGCATGACGACGACACACCTCTCTGCTGAGG 348

RESULT 12

US-10-972-50806/c
Sequence 50806, Application US/10972079
Publication No. US2005015317A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: KERR, Richard
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEE
FILE REFERENCE: NM1110-2
CURRENT APPLICATION NUMBER: US/10/972.079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50806
LENGTH: 574
TYPE: DNA
ORGANISM: Chicken
US-10-972-50806

Query Match 23.6%; Score 36.4; DB 9; Length 574;
Best Local Similarity 56.8%; Pred. No. 0.037;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 7 GTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAAATGGGC 66
DB 471 GTGCTGCTCTGAAGTCCACACTGAAACAATTGACCTACTCATGTCCCTTAAATGGGC 412
QY 67 AAACATTGCAAGCAGCAAAACAGCAACACAGCCCTCTGCTGACCTTGGAG 124
DB 411 GCACTGCGCAGCAGCGCATCTGCATGACGACGACACACCTCTCTGCTGAGG 354

RESULT 13

US-09-925-065A-103590
Sequence 103590, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103590
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-103590

Query Match
Best Local Similarity 58.9%; Score 32.6; DB 4; Length 645;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

57 TAAATGGGCAACATTGCAAGCAGCAACAGCAAGCCCTCCCTGCTGCA 116
65 TGAATAGGGGAGAAATGATGAGATTAACCAAGACAGAGCAGATTCCTGCGAGA 124

117 CCTTGAGCTGGGCGAGAGCTCAGAGACCTCTG 151
125 GCCTGTAGAGGTAAAGAGTCATATTTATTTCTG 159

RESULT 14
US-09-925-065A-103589
; Sequence 103589, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103589
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-103589

Query Match
Best Local Similarity 57.9%; Score 32.2; DB 4; Length 645;
Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

57 TAAATGGGCAACATTGCAAGCAGCAACAGCAAGCCCTCCCTGCTGCA 116
65 TGAATAGGGGAGAAATGATGAGATTAACCAAGACAGAGCAGATTCCTGCGAGA 124

117 CCTTGAGCTGGGCGAGAGCTCAGAGACCTCTG 151
125 GCCTGTAGAGGTAAAGAGTCATATTTATTTCTG 159
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RESULT 15
US-09-925-065A-782496/c
; Sequence 782496, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 782496
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-782496

Query Match
Best Local Similarity 51.8%; Score 31.8; DB 4; Length 662;
Matches 72; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

11 TGCTGTGAGTCCACACTGAGCAAACTTCAGCCTACTCATATGCTTAAATGGGCAAC 70
141 TGCACCTGCACTCCAGACTGAGTGAAGCAGAGCACTCACTCTTAAAGAAAG 82

71 ATTGCAAGCAGCAACAGCAACAGCAAGCCCTCCCTGCTGCTGAGCTGGAGCTGGG 130
81 AAAAGAAAGAAAGAAATGAGCACTCATATGCTGCTCCCTGAGTCTGGAGCTGGCC 22

131 CAGAGTCAAGAGCCTCTC 149
21 AGAGAGAGGAGCCCTCC 3

Db
```

Search completed: April 18, 2006, 13:17:10
Job time : 155.338 secs

RESULT 2
US-10-995-561-13467
; Sequence 13467, Application US/10995561

```
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13467
LENGTH: 16963
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-13467

Query Match      100.0%; Score 154; DB 8; Length 16963;
Best Local Similarity 99.4%; Pred. No. 2,1e-39;
Matches 153; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 60
DB 15958 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 16017
QY 61 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 120
DB 16018 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 16077
QY 121 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 154
DB 16078 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 16111

RESULT 3
US-10-995-561-13513
Sequence 13513, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13513
LENGTH: 40000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1) ... (40000)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13513

Query Match      100.0%; Score 154; DB 8; Length 40000;
Best Local Similarity 99.4%; Pred. No. 2,8e-39;
Matches 153; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 60
DB 38766 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 38825
QY 61 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 120
DB 38826 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 38885
QY 121 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 154
DB 38886 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 38919
```

```
RESULT 4
US-10-995-561-75740
Sequence 75740, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75740
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-75740

Query Match      95.2%; Score 146.6; DB 8; Length 201;
Best Local Similarity 99.3%; Pred. No. 8,7e-38;
Matches 146; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 60
DB 55 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 114
QY 61 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 120
DB 115 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 174
QY 121 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 147
DB 175 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 201

RESULT 5
US-10-995-561-84658
Sequence 84658, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 84658
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-84658

Query Match      95.2%; Score 146.6; DB 8; Length 201;
Best Local Similarity 99.3%; Pred. No. 8,7e-38;
Matches 146; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 60
DB 55 GTTGTGTGCTGCTCTGAAGTCCAGCTGAACAACTTCAAGCTTCAATGTCCTTAA 114
QY 61 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 120
DB 115 ATGGGCAAACTTGCAGACGCAAAACAGCAACACAGAGCCCTCCCTGCTGACCTT 174
QY 121 GGAGCTGGGGGCAAGGTCAAGACCTCTCTGGGC 147
```

Db 175 GGAGCTGGGGCAGAGTCAAGACCTC 201

RESULT 6

US-10-301-480-203835
; Sequence 203835, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203835
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-203835

Query Match 21.2%; Score 32.6; DB 9; Length 625;

Best Local Similarity 58.9%; Pred. No. 1.7;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 57 TAAATGGGCAACATTGCAAGCAGCAACAGCAACAGCCCTCCCTGCTGCA 116
Db 45 TGAAGGGGGAATGATGAGATTAATCTCAAGCAGAGCAGAGTTCCTGCAGA 104

Qy 117 CCTTGAAGCTGGGGCAGAGTCAAGACCTCTCTG 151
Db 105 GCCTTGAAGGTAAAGAGTCAATATTTATTTCTG 139

RESULT 7

US-10-301-480-817244
; Sequence 817244, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817244
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-817244

Query Match 21.2%; Score 32.6; DB 10; Length 625;

Best Local Similarity 58.9%; Pred. No. 1.7;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 57 TAAATGGGCAACATTGCAAGCAGCAACAGCAACAGCCCTCCCTGCTGCA 116
Db 45 TGAAGGGGGAATGATGAGATTAATCTCAAGCAGAGCAGAGTTCCTGCAGA 104

Qy 117 CCTTGAAGCTGGGGCAGAGTCAAGACCTCTCTG 151
Db 105 GCCTTGAAGGTAAAGAGTCAATATTTATTTCTG 139

RESULT 8

US-09-925-065A-103590
; Sequence 103590, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103590
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-103590

Query Match 21.2%; Score 32.6; DB 6; Length 645;

Best Local Similarity 58.9%; Pred. No. 1.8;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 57 TAAATGGGCAACATTGCAAGCAGCAACAGCAACAGCCCTCCCTGCTGCA 116
Db 65 TGAAGGGGGAATGATGAGATTAATCTCAAGCAGAGCAGAGTTCCTGCAGA 124

Qy 117 CCTTGAAGCTGGGGCAGAGTCAAGACCTCTCTG 151
Db 125 GCCTTGAAGGTAAAGAGTCAATATTTATTTCTG 159

RESULT 9

US-10-301-480-203834
; Sequence 203834, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203834
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-203834

Query Match 20.9%; Score 32.2; DB 9; Length 625;

Best Local Similarity 57.9%; Pred. No. 2.4;
Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 57 TAAATGGGCAACATTGCAAGCAGCAACAGCAACAGCCCTCCCTGCTGCA 116
Db 117 CCTTGAAGCTGGGGCAGAGTCAAGACCTCTCTG 151

Db 45 TGAAGGGGAGAAATTGATGAGATTAACCTCAAGACAGAGGAGGAGGATTCTTGACA 104

Qy 117 CTTGAGAGCTGGGCGAGAGGCTCAGAGACCTCTCTG 151

Db 105 GCCTTGTAGAGGTAAAGAGGCTCATATTTATTCTG 139

RESULT 10
US-10-301-480-817243

Sequence 817243, Application US/10301480
Publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 817243

LENGTH: 625

TYPE: DNA

ORGANISM: Homo sapiens

US-10-301-480-817243

Query Match

Best Local Similarity 57.9%; Pred. No. 2.4;

Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 57 TAAATGGGCAACATTGCAAGCAAGCAACAGCAACAGCCTCTCTGCTCTGA 116

Db 45 TGAAGGGGAGAAATTGATGAGATTAACCTCAAGACAGAGGAGGATTCTTGACA 104

Qy 117 CTTGAGAGCTGGGCGAGAGGCTCAGAGACCTCTCTG 151

Db 105 GCCTTGTAGAGGTAAAGAGGCTCATATTTATTCTG 139

RESULT 11
US-09-925-065A-103589

Sequence 103589, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 103589

LENGTH: 645

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-103589

Query Match

Best Local Similarity 20.9%; Score 32.2; DB 6; Length 645;

Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Best Local Similarity 57.9%; Pred. No. 2.4;

Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 57 TAAATGGGCAACATTGCAAGCAAGCAACAGCAACAGCCTCTCTGCTCTGA 116

Db 65 TGAAGGGGAGAAATTGATGAGATTAACCTCAAGACAGAGGAGGATTCTTGACA 124

Qy 117 CTTGAGAGCTGGGCGAGAGGCTCAGAGACCTCTCTG 151

Db 125 GCCTTGTAGAGGTAAAGAGGCTCATATTTATTCTG 159

RESULT 12
US-09-925-065A-782496/C

Sequence 782496, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 782496

LENGTH: 662

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-782496

Query Match

Best Local Similarity 51.8%; Pred. No. 3.3;

Matches 72; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 11 TGGCTGAGAGCTGACAGCTGAACTTGAAGCTTACTATGCTTAAATGGGCAAC 70

Db 141 TGGCTGAGAGCTGACAGCTGAACTTGAAGCTTACTATGCTTAAATGGGCAAC 82

Qy 71 ATTGCAAGCAGCAACAGCAACAGCAACAGCCTCTCTGCTCTGACTTGGAGCTGGG 130

Db 81 AAAAGAAAAAAGAAATGAGAGCTCATATCTGCTTCCCTGAGATCTGGAGCTGGCC 22

Qy 131 CAGAGGCTCAGAGACCTCTCTC 149

Db 21 AGAGAGGAGGAGGCTCTCC 3

RESULT 13
US-11-124-367A-5038

Sequence 5038, Application US/11124367A
Publication No. US20060024700A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

FILE REFERENCE: CL001519.ORD

CURRENT APPLICATION NUMBER: US/11/124,367A

PRIOR FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,846

PRIOR FILING DATE: 2004-05-07

PRIOR APPLICATION NUMBER: US 60/582,609

Query Match

Best Local Similarity 20.6%; Score 31.8; DB 6; Length 662;

Matches 72; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5038
; LENGTH: 24675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5038

Query Match
Best Local Similarity 55.5%; Pred. No. 13;
Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2 TTTGTGCTGCTGCTGAGTCCAGCTGAAACAATTGACCTACTCATGTCCCTTAAA 61
Db 18177 TTTGCAAGCTGCTGCTGCTGAGTCCAGCTGAAACAATTGACCTACTCATGTCCCTTAAA 18236

QY 62 TGGGCAACATTGCAAGCAGCAACCAACACACACAGCCCTCCCTGCT 111
Db 18237 AGTACTTACGTTGCAATCAGCAAGATGCAACAAACATCTCTCCACCT 18286

RESULT 14
US-09-925-065A-370446/c
; Sequence 370446, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370446
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-370446

Query Match
Best Local Similarity 20.3%; Score 31.2; DB 6; Length 611;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 4 TGTGTGCTGCTGCTGAGTCCAGCTGAAACAATTGACCTACTCATGTCCCTTAAA 63
Db 197 TTTTGCATTCACATTCGTCAGATGCTAAGTTGAGCATATGCTTCCCAAAAGTG 138

QY 64 GGCACACATTGCAAGCAGCAACCAACACACACAGCCCT 103
Db 137 GACACACACACACACACACACACACACACATACACACAT 98

RESULT 15
US-09-925-065A-370447/c
; Sequence 370447, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

```

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370447
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-370447

Query Match
Best Local Similarity 20.3%; Score 31.2; DB 6; Length 611;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 4 TGTGTGCTGCTGCTGAGTCCAGCTGAAACAATTGACCTACTCATGTCCCTTAAA 63
Db 197 TTTTGCATTCACATTCGTCAGATGCTAAGTTGAGCATATGCTTCCCAAAAGTG 138

QY 64 GGCACACATTGCAAGCAGCAACCAACACACACAGCCCT 103
Db 137 GACACACACACACACACACACACACACACATACACACAT 98
```

Search completed: April 18, 2006, 15:39:40
Job time : 95.5846 secs

OY 121 GGAGCTGGGAGAGGTGAGAGCTCTGTGGGC 154
DB 201 GGAGCTGGGAGAGGTGAGAGCTCTGTGGGC 234

RESULT 2

US-09-001-039B-61
Sequence 61, Application US/09001039B
Patent No. 6818439

GENERAL INFORMATION:

APPLICANT: Jolly, Douglas J.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Respass, James G.
APPLICANT: Depolo, Nicholas J.
APPLICANT: Hsu, David Chi-Tang
APPLICANT: Ibanez, Carlos E.
APPLICANT: Greengard, Judith

APPLICANT: Lee, Will

TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/001,039B

FILING DATE: 13-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-001-039B-61

Query Match 53.2%; Score 82; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTGTGTGCTGCTCTGAAGTCACAGTGAACAACCTTACCTCTATGTCCTTAA 60
DB 9 GTTGTGTGCTGCTCTGAAGTCACAGTGAACAACCTTACCTCTATGTCCTTAA 68

OY 61 ATGGGCAACATTCGCAAGCAGC 82
DB 69 ATGGGCAACATTCGCAAGCAGC 90

RESULT 3

US-09-001-039B-65

Sequence 65, Application US/09001039B

Patent No. 6818439

GENERAL INFORMATION:

APPLICANT: Jolly, Douglas J.

APPLICANT: Chang, Stephen M.W.
APPLICANT: Respass, James G.
APPLICANT: Depolo, Nicholas J.
APPLICANT: Hsu, David Chi-Tang
APPLICANT: Ibanez, Carlos E.
APPLICANT: Greengard, Judith

APPLICANT: Lee, Will

TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/001,039B

FILING DATE: 13-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-001-039B-65

Query Match 53.2%; Score 82; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTGTGTGCTGCTCTGAAGTCACAGTGAACAACCTTACCTCTATGTCCTTAA 60
DB 9 GTTGTGTGCTGCTCTGAAGTCACAGTGAACAACCTTACCTCTATGTCCTTAA 68

OY 61 ATGGGCAACATTCGCAAGCAGC 82
DB 69 ATGGGCAACATTCGCAAGCAGC 90

RESULT 4

US-09-001-039B-67/C

Sequence 67, Application US/09001039B

Patent No. 6818439

GENERAL INFORMATION:

APPLICANT: Jolly, Douglas J.

APPLICANT: Chang, Stephen M.W.

APPLICANT: Respass, James G.

APPLICANT: Depolo, Nicholas J.

APPLICANT: Hsu, David Chi-Tang

APPLICANT: Ibanez, Carlos E.

APPLICANT: Greengard, Judith

APPLICANT: Lee, Will

TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001.039B
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
US-09-001-039B-67
Query Match 50.6%; Score 78; DB 3; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 22 GGTGAGAGACCTCTCTG 5
QY 135 GGTGAGAGACCTCTCTG 152
DB 82 CAGACGCAACAGCAACAGACGACCTCTCTGAGCTTGAGCTGGGGCAGA 23
QY 75 CAGACGCAACAGCAACAGACGACCTCTCTGAGCTTGAGCTGGGGCAGA 134
DB 82 CAGACGCAACAGCAACAGACGACCTCTCTGAGCTTGAGCTGGGGCAGA 23
DB 22 GGTGAGAGACCTCTCTG 5
RESULT 5
US-09-001-039B-63/C
Sequence 63, Application US/09001039B
Patent No. 6818439
GENERAL INFORMATION:
APPLICANT: Jolly, Douglas J.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Respass, James G.
APPLICANT: Depolo, Nicholas J.
APPLICANT: Hsu, David Chi-Tang
APPLICANT: Ibanez, Carlos E.
APPLICANT: Greengard, Judith
APPLICANT: Lee, Will
TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001.039B
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
US-09-001-039B-63

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001.039B
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
US-09-001-039B-63
Query Match 50.0%; Score 77; DB 3; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.4e-16;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 22 GGTGAGAGACCTCTCTG 6
QY 135 GGTGAGAGACCTCTCTG 151
DB 82 CAGACGCAACAGCAACAGACGACCTCTCTGAGCTTGAGCTGGGGCAGA 23
QY 75 CAGACGCAACAGCAACAGACGACCTCTCTGAGCTTGAGCTGGGGCAGA 134
DB 82 CAGACGCAACAGCAACAGACGACCTCTCTGAGCTTGAGCTGGGGCAGA 23
DB 22 GGTGAGAGACCTCTCTG 6
RESULT 6
US-09-001-039B-64/C
Sequence 64, Application US/09001039B
Patent No. 6818439
GENERAL INFORMATION:
APPLICANT: Jolly, Douglas J.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Respass, James G.
APPLICANT: Depolo, Nicholas J.
APPLICANT: Hsu, David Chi-Tang
APPLICANT: Ibanez, Carlos E.
APPLICANT: Greengard, Judith
APPLICANT: Lee, Will
TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001.039B
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

Query Match 48.1%; Score 74; DB 3; Length 78;

Qy	143	ACCTCTCTGG	15
Db	61	ACCTCTCTGG	70

RESULT 9
US-09-001-039B-62
Sequence 62, Application US/09001039B
Patent No. 6818439
GENERAL INFORMATION:
APPLICANT: JOLLY, Douglas J.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Respass, James G.
APPLICANT: DePolo, Nicholas J.
APPLICANT: Hsu, David Chi-Tang
APPLICANT: Ibanez, Carlos E.
APPLICANT: Greengard, Judith
APPLICANT: Lee, Will
TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001.039B
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-001-039B-62
Query Match 44.8%; Score 69; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.7e-13;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 AAACAGCAACACAGCCTCTGCTGCTGACCTTGACCTGGGGCAGAGGTCAAG 142
DB 1 AAACAGCAACACAGCCTCTGCTGCTGACCTTGACCTGGGGCAGAGGTCAAG 60

QY 143 ACCTCTCTG 151
DB 61 ACCTCTCTG 69

RESULT 10
US-09-799-451-433/C
Sequence 433, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan

APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yundong
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 433
LENGTH: 2018
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1746)
US-09-799-451-433
Query Match 20.1%; Score 31; DB 3; Length 2018;
Best Local Similarity 62.0%; Pred. No. 3.5;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 33 CAACCTGACCTGATCTATCTCCCTAAATGGGCAACATTGCAGACGCAAGCAAA 92
DB 1917 CACAGTGGCCTCATCATCATCTCGAATAGCGCATCTCTGGAGTGGCTGTGCACT 1858

QY 93 CACACAGCCTCCCTGCT 111
DB 1857 CACCCAGCCCCCTGCGCT 1839

RESULT 11
US-09-949-016-17561
Sequence 17561, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1801307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17561
LENGTH: 113379
TYPE: DNA
ORGANISM: Human
US-09-949-016-17561
Query Match 20.1%; Score 31; DB 3; Length 113379;
Best Local Similarity 56.3%; Pred. No. 15;
Matches 58; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 12 GCCTGTGAGTCCACACGCAACAACTTCAAGCCTTACTATGTCCCTAAATGGCAACA 71
DB 113379 GCCTGTGAGTCCACACGCAACAACTTCAAGCCTTACTATGTCCCTAAATGGCAACA 71

```

Query Match Summary: 20.1%; Score 31; DB 3; Length 113379;
Best Local Similarity: 56.3%; Pred. No. 15;
Matches 58; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY      12  GCCTGTGAAGTCCACACTGAACAACTTCAGCCTACTCATGTCCCTAAATGGGCAAAACA 71
Db      67313  GCCTTTGAAACCCCTTCCTGTAATAGTGTGTACAGACAAATGATTTTGAATATAAATGGACAAT 67372
QY      72  TTGCAAGCAAGCAACAGCAACGACACAGCCCTCCCTGCTCT 114
Db      67373  AGGCAAGCAACATTAATGAACTAGTCATAAAGTACTTAAGTCT 67415

RESULT 13
PCT-US93-06251-23/C
: Sequence 23, Application PC/TUS9306251.
: GENERAL INFORMATION:
: APPLICANT: Wickstrom, Eric and Rife, Jason P.
: TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
: TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
: NUMBER OF SEQUENCES: 93
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: NY
: COUNTRY: USA
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/06251
: FILING DATE: 19930630
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Digiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 8586

```

	Query Match	Best Local Similarity	19.7%;	Score 30.4;	DB 6;	Length 11558;
	Matches	70;	Conservative	0;	Mismatches	66;
					Indels	0;
					Gaps	0;
QY	9	GCTGCCTCTGAAGTCACACTGAACAACTTCAGCCTACTCATGTCCCTTAAATGGGCAA	68			
Db	9728	GCCCCCTCCAGAGCTCCAGACTTGGGCCCTCTTCAGTTCCCACTGGACCCCTCATTTGACCTG	9669			
QY	69	ACATTGCACACACAAACACAAACACACAGCCCTCCCTGCCCTGCACCTTGGAGCTGG	128			
Db	9668	GCTCTGGAAATAGCTGAGAACCCAGACGCGGGAACGACGGGCAAGAGGCTCAAGAGGAGAA	9609			
QY	129	GGCAGAGGTCAAGAC	144			
Db	9608	GTCAGAGTCAAGAGCC	9593			

```

Sequence 15347, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15347
LENGTH: 80706
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(80706)
OTHER INFORMATION: n = A,T,C or G
IS-09-949-016-15347

```

Query Match	19.6%	Score 30.2	DB 3	Length 80706
Best Local Similarity	55.1%	Pred. No. 24		
Matches	59	Conservative	0	Mismatches 48; Indels 0; Gaps 0;
QY	47	CTCATGTCCCTTAATAATGGGCAACATTGCGACGACGAAACAGCAACACAGCCCTCC	106	
Db	35087	CAACTCTCCCTGGAGTACAGAGAAATCTTCCAGGCATCTGCGCCAGACCCAGCCTCGAGC	35144	
QY	107	TGCGCTGTGACCTTGGAGCTGGGGCGAGAGATCGAGACCTCTCTGGG	153	
Db	35147	AGCTGGCAACAGAGAGGAGCGGGGAATGTGTGGCTTATCTCTCTGGG	35193	
RESULT	15			

```

US-09-669-751-144/C
Sequence 144, Application US/09669751
Patent No. 6551575
GENERAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
TITLE OF INVENTION: Balance and the Perception of Gravity
FILE REFERENCE: P-NI 3864
CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 144
LENGTH: 658
TYPE: DNA
ORGANISM: Drosophila
US-09-669-751-144

```

Query Match	19.5%	Score 30	DB 3	Length 658
Best Local Similarity	53.4%	Pred. No. 5		
Matches 63	Conservative 0	Mismatches 55	Indels 0	Gaps 0

QY CTGCTCTGAAGTCCACATGAAACAACTTGAGCCCTACTCATGTCCCTAAATGGGAAA 69
10 CTGCTCTGAAGTCCACATGAAACAACTTGAGCCCTACTCATGTCCCTAAATGGGAAA 69
Db CTGATTTCTGATCAAGATTCTGATCAAGATTCTGATCAAGATTCTGATCAAGATTCTGATA 333
QY 70 CATTGCAAGACGAAACAGCAACACAGCCCTCCCTGCTGCTGACCTTGAGCTG 127
Db 332 CATTCTTCATTAATAGTCTGCAAGGGCTTGACCTGCTGCCAGATTATTTGAGCCG 275

Search completed: April 18, 2006, 12:30:28
Job time : 34.8522 secs